

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 09:28:05 ; Search time 7690.28 Seconds  
 10963.461 Million cell updates/sec

Title: US-10-712-479-3

Perfect score: 1

Sequence: 1 agcctgacgacgcacgc.....gcacccaccacccacac 1740

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits selected chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01

Maximum Match 1001

Listing first 45 summaries

Database :

GenBank:

1: gb\_ba.\*

2: gb\_ba.\*

3: gb\_ba.\*

4: gb\_ba.\*

5: gb\_ov.\*

6: gb\_ov.\*

7: gb\_ov.\*

8: gb\_ov.\*

9: gb\_ov.\*

10: gb\_ov.\*

11: gb\_ov.\*

12: gb\_ov.\*

13: gb\_ov.\*

14: gb\_ov.\*

Prod. No. is the number of results predicted by chance to have a score as high as the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	1585.4	91.1	9547	14	AB049091			AB049091 Hepatitis C
2	1582.2	90.9	9379	14	D89515			D89515 Hepatitis C
3	1574.2	90.5	9379	14	AF165039			AF165039 Hepatitis C
4	1572.6	90.4	9379	14	AF165060			AF165060 Hepatitis C
5	1572.6	90.4	9379	14	AB057599			AB057599 Hepatitis C
6	1572.6	90.4	9379	14	AB049091			AB049091 Hepatitis C
7	1565.8	89.8	9379	14	AF207767			AF207767 Hepatitis C
8	1565.8	89.8	9379	14	AF207767			AF207767 Hepatitis C
9	1561.4	89.7	9379	14	AF207767			AF207767 Hepatitis C
10	1559.8	89.6	9379	14	AF207767			AF207767 Hepatitis C
11	1558.2	89.6	9379	14	AF207767			AF207767 Hepatitis C
12	1558.2	89.6	9379	14	AF207767			AF207767 Hepatitis C
13	1554.8	89.3	9379	14	AF165062			AF165062 Hepatitis C
14	1553.8	89.3	1773	14	AB057601			AB057601 Hepatitis C
15	1553.4	89.3	1743	6	AX686768			AX686768 Sequence
16	1553.4	89.3	1743	6	BD010839			BD010839 HCV poly
17	1552.2	89.2	9379	14	AF207767			AF207767 Hepatitis C
18	1551.8	89.2	9414	14	HCU16352			HCU16352 Hepatitis C
19	1551.8	89.2	9415	14	HCU16352			HCU16352 Hepatitis C

20	1551.8	89.2	9460	14	AB049097			AB049097 Hepatitis C
21	1551.8	89.2	9460	14	AF013390			AF013390 Sequence
22	1549.8	89.1	9435	14	AB049093			AB049093 Hepatitis C
23	1549.8	89.1	9435	14	AF207756			AF207756 Hepatitis C
24	1549.2	89.0	9535	14	D85516			D85516 Hepatitis C
25	1549.2	89.0	9535	14	AF044867			AF044867 Hepatitis C
26	1548.6	89.0	9537	14	AB031322			AB031322 Hepatitis C
27	1548.4	89.0	1773	14	AB031322			AB031322 Hepatitis C
28	1548.4	89.0	1773	14	AB057680			AB057680 Hepatitis C
29	1547.8	88.9	9460	14	HFC0481			HFC0481 Sequence
30	1547.8	88.9	9460	14	AF054247			AF054247 Sequence
31	1547.8	88.9	9555	14	AF054247			AF054247 Sequence
32	1547.8	88.9	9555	14	AF054247			AF054247 Sequence
33	1546.8	88.9	9573	14	AB049090			AB049090 Hepatitis C
34	1546.8	88.9	9573	14	AF054248			AF054248 Hepatitis C
35	1546.8	88.9	9573	14	AF054248			AF054248 Hepatitis C
36	1543.8	88.7	9379	14	AF207767			AF207767 Hepatitis C
37	1543.8	88.7	9379	14	AF207767			AF207767 Hepatitis C
38	1543.8	88.7	9587	14	AF333324			AF333324 Hepatitis C
39	1543.8	88.7	1773	14	AB057602			AB057602 Hepatitis C
40	1543.8	88.7	1773	14	AF165061			AF165061 Hepatitis C
41	1542.2	88.6	9379	14	AF165058			AF165058 Hepatitis C
42	1542.2	88.6	9446	14	HCU11214			HCU11214 Hepatitis C
43	1542.2	88.6	9596	14	AF054249			AF054249 Hepatitis C
44	1542.2	88.6	9596	14	AF054249			AF054249 Hepatitis C
45	1540.8	88.6	9359	14	AF313916			AF313916 Hepatitis C

## ALIGNMENTS

AB049091	C virus gene for polyprotein, complete cde,	9547 bp	RNA	linear	VFL 22-AUG-2002
Isolate:HCV1142					
AB049091.1	GI:11559448				
Hepatitis C virus					
Hepatitis C virus					
Viruses; asRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepavirinae.					
Takahashi,K., Iwata,K., Matsumoto,M., Matsumoto,H., Nakao,K., Hasegawa,T., Ohta,Y., Kuno,K., Nishio,H., Baba,K., Fujikata,M. and Minato,S. J. Clin. Virol. 40:1-3 (2001)					
Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited					
1148851	Ref. 2 (2), 161-171 (2001)				
2 (bases 1 to 9547)					
Mishiro,S					
Mishiro,S					
Submitted (19-SEP-2000) Shunji Mishiro, Toshiba General Hospital, Department of Medical Sciences, 6-3-22 Higashi Oh, Shinjuku, Tokyo 140-8522, Japan (E-mail:shunji.mishiro@toshiba.co.jp, Tel:81-3-3764-8981, Fax:81-3-3764-8992)					
1					
Location/Qualifiers					
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/db_xref="taxon:11103"					
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/note="HCV-genotype: 1b"					
41..259					
260..9392					
5'UTR					
CDS					
/codon_start=1					
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/protein_id="BAB18804.1"					





[illegible]















DB	7587	TCAGTGTCTTACACATGACGACGATGCCCTTGATCTACACATATCCCTCGCGAGAGAGACAA	7614
OY	73	CTCCCACTCAAGCGCGCTGAGCAACTCTCTTGCTGGTGCACATAAATCTGCTATTCCACA	132
DB	7647	CTCCCACTCAAGCGCGCTGAGCAACTCTCTTGCTGGTGCACATAAATCTGCTATTCCACA	7768
OY	133	ACATCCCGATCCGATGACATGCTGCGGACGAGAGAGATCACTTTCAGATCGATGTCGCG	192
DB	7707	ACATCCCGATGCTAGCGCTCGCGGACGAGAGAGATCACTTTCAGATCGATGTCGCG	7768
OY	193	GAGGATATATATATCCGAGGCGCTCTGAGAGATGAGAGAGGCGCTCACAGTGAAGGCT	252
DB	7767	GAGGACCACTATCCGAGGCGCTCTGAGAGATGAGAGAGGCGCTCACAGTGAAGGCT	7828
OY	253	AAATCTGCATCTCTGAGAGAGACATCCAGATGATGCGCCCTGGCATTGGCGCAATCCAA	312
DB	7827	AAATCTGCATCTCTGAGAGAGACATCCAGATGATGCGCCCTGGCATTGGCGCAATCCAA	7888
OY	313	TATGTGCTATGTGGGCAAGAGAGCTCTCGGAGCTATCTCAGACGAGCGCTTACCCATCCG	37
DB	7887	TATGTGCTATGTGGGCAAGAGAGCTCTCGGAGCTTACCCATCCGAGCGCTTACCCATCCG	7948
OY	373	TCGCTGTGTGAGAGATCTGTGTGACACATGACACATCCATATGACGACGACGACGAC	432
DB	7947	TCGCTGTGTGTGAGAGATCTGTGTGACACATGACACATCCATATGACGACGACGACGAC	8006
OY	433	AAATATGAGTCTTCTGCTGCATCCAGACGAGAGAGGCGTGGAAAGCTGCTCATC	492
DB	8007	AAATATGAGTCTTCTGCTGCATCCAGACGAGAGAGGCGTGGAAAGCTGCTCATC	8066
OY	493	GTATCTCCGAGCTCGGAGGCTGTGTGTATGTGAGAGATGAGGCTTTAGAGCGTGTTTC	552
DB	8067	GTATCTCCGAGCTCGGAGGCTGTGTGTATGTGAGAGATGAGGCTTTAGAGCGTGTTTC	8126
OY	553	ACTCTCTCTCAAGCGCTGATAGGGGCTCTCTATAGGATTCATATCTCTTCAAGCGCG	612
DB	8127	ACTCTCTCTCAAGCGCTGATAGGGGCTCTCTATAGGATTCATATCTCTTCAAGCGCG	8186
OY	613	CTCTGAGGCTCTGCTGATGACCTCGAGAGCAAGCAATCCCTCATGGGCTCATGATGAC	672
DB	8187	CTCTGAGGCTCTGCTGATGACCTCGAGAGCAAGCAATCCCTCATGGGCTCATGATGAC	8246
OY	673	ACCGCTGTGTGTATGATCTCATGAGCTCTGAGATATCATCTCTGTGTGAGAGTCAATTAC	732
DB	8247	ACCGCTGTGTGTATGATCTCATGAGCTCTGAGATATCATCTCTGTGTGAGAGTCAATTAC	8306
OY	733	CAATGTGTGTGACTTGGGCTCCGACAGCTGAGCAGGCGCATAGGCTGCTTCACAGAGCGGCT	792
DB	8307	CAATGTGTGTGACTTGGGCTCCGACAGCTGAGCAGGCGCATAGGCTGCTTCACAGAGCGGCT	8366
OY	793	TATGTGTGGGGTCTCCATGATTAATCTCAAAAGGCGAGCTGAGCTATCTGCGGCTCGCG	852
DB	8367	TATGTGTGGGGTCTCCATGATTAATCTCAAAAGGCGAGCTGAGCTATCTGCGGCTCGCG	8426
OY	853	CGCAGGCGGCTCTGAGGATGAGCTGGGCTTATCTCTCATATCTCATGTGAGAGCGGCT	912
DB	8427	CGCAGGCGGCTCTGAGGATGAGCTGGGCTTATCTCTCATATCTCATGTGAGAGCGGCT	918
OY	913	GCAGCTGTGATCTGCACTGACATGACATGACATGACATGATCTGTGATGTGAGAGTCACTT	972
DB	9187	GCAGCTGTGATCTGCACTGACATGACATGACATGACATGATCTGTGATGTGAGAGTCACTT	978
OY	973	GTGCTTATCTGTGAGAGCGCGGAGAACCAAGGACAGCGGAGAGCTACAGATCTTCAAGC	1032
DB	9547	GTGCTTATCTGTGAGAGCGCGGAGAACCAAGGACAGCGGAGAGCTACAGATCTTCAAGC	9606
OY	1033	GAGGCTATGACTAGGTAATCTTGCCTCCCTCTGGGAGAGCGCCCAACCGAATACAGCTTG	1092
DB	8607	GAGGCTATGACTAGGTAATCTTGCCTCCCTCTGGGAGAGCGCCCAACCGAATACAGCTTG	8666
OY	1093	GAGGCTATGACTAGGTAATCTTGCCTCCCTCTGGGAGAGCGCCCAACCGAATACAGCTTG	1152
DB	8667	GAGGCTATGACTAGGTAATCTTGCCTCCCTCTGGGAGAGCGCCCAACCGAATACAGCTTG	8726

[illegible][illegible]

















[illegible][illegible]

DPRIEVDYLIITGSCSVSVVADSGKVVYLTDRDTPPLARMAETABTBSWML  
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 GLSAYLSHVSPEIINVSASCLKIVLPVVRHRAVRVAKLLSDGGRAATCKYTL  
 FPMVAETKCTKTPIPASGLDILSSNFIAGVSGDITYHSLSHSPNFMULCILLISGVV  
 GNYLIPNR\*

ORIGIN Query Match 89.3%; Score 1554; DB 14; Length 9719;  
 Best Local Similarity 94.2%; Pred. No. 0;  
 Matches 1614; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 8 GCATGTCATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 67  
 DB 7582 CTGCTTGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 7641  
 DB 68 GCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 127  
 DB 7642 GCAATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 7701  
 DB 128 CACACATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 187  
 DB 7702 CACACATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 7761  
 QY 188 TCCTGCAATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 197  
 DB 7762 TCCTGCAATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 7821  
 QY 248 AGCTGAAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 307  
 DB 7822 AGCTGAAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 7881  
 QY 308 CCAATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 367  
 DB 7882 CCAATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 7941  
 QY 368 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 427  
 DB 7942 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8001  
 QY 428 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 487  
 DB 8002 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8061  
 QY 488 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 547  
 DB 8062 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8121  
 QY 548 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 607  
 DB 8122 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8181  
 QY 608 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 667  
 DB 8182 TCGATGTCGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8241  
 QY 668 ATGACACCGCTGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 727  
 DB 8242 ATGACACCGCTGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8301  
 QY 728 TTATGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 787  
 DB 8302 TTATGCAATGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8361  
 QY 788 GCTTATGCTGCGGGGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 847  
 DB 8362 GCTTATGCTGCGGGGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8421  
 QY 848 GCGCGCGCGCGCGCTGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 907  
 DB 8422 GCGCGCGCGCGCGCTGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 8481  
 QY 908 CGCTGCGCGCGCGCTGCTTACATGACGAGCGCCCTGATCACAGCTGCTGGAGAAA 967

8482 CTTCTGAGCTGTGTCGAGCTGCAAGCTCCAGAGCTCGAGACTGCGTGTGAACGAGACG 8541  
 QY 968 ACTCTGCTGTTATGTATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077  
 DB 8542 ACTCTGCTGTTATGTGAG 8601  
 QY 1077 TCAAG 1087  
 DB 8602 TCAAG 8661  
 QY 1147 ACTGAG 1147  
 DB 8662 ACTGAG 8721  
 QY 1207 AAG 1207  
 DB 8721 AAG 8781  
 QY 1267 CAG 1267  
 DB 8782 CAG 8841  
 QY 1327 TGTGAG 1327  
 DB 8842 TGTGAG 8901  
 QY 1387 TGTGAG 1387  
 DB 8902 TGTGAG 8961  
 QY 1447 TGTGAG 1447  
 DB 9021 TGTGAG 9021  
 QY 1507 TGTGAG 1507  
 DB 9082 TGTGAG 914  
 QY 1568 TGTGAG 1568  
 DB 9142 TGTGAG 920  
 QY 1628 TGTGAG 1628  
 DB 9202 TGTGAG 926  
 QY 1688 TGTGAG 1721  
 DB 9262 TGTGAG 9295

RESULT 14  
 LOCUS AB057601  
 DEFINITION Hepatitis C virus gene for RNA polymerase, partial cds, clone pnt. 4.  
 ACCESSION AB057601.1  
 VERSION GI.29466628  
 KEYWORDS Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REPEATS 1  
 AUTHORS Matanabe K. and Yoshioka K.  
 TITLE Mutagenesis of the NS5B  
 REFERENCE 1  
 2. (bases 1 to 173)  
 AUTHORS Matanabe K., Yoshioka K., Yano M., Ukai K. and Ito H.







[illegible]

Search completed: October 3, 2005, 18:55:33  
Job time : 7694.28 secs

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[illegible]

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK plate: 86 Row: 0 Column: 1  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA q1: 9624972  
 This clone has the following problem: frame shifted.

## FEATURES

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/clone_lib="NIH MGC_94"
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Matches 114; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

309 CAAATTGGCTATGGGCAAGGAGCTCCGGAGCCTATCCAGCAGGGCCGTTACACAT 368  
4435 CCATCTTGGCGAGAGTTTCAGAGGACAGCTCCCGCATCTCTATCACTGTTTGGCCTCTT 4494

369 CCGTCCGTGTGGAAGCACTTGCTGGAGGACACTGACACCACTTACAGCCACATCAT 428  
4495 CCGAGTCATGAGCGTGTCAAGCTTCTGAGTAGGGGTAGGGGATCCGCACTGTCTGTG 4554

429 GGCAAAATGAGGTTTCTGGTCCAACAGAGAAAGGAGCGCAACACGCTCGCT 488  
4555 GACATTCATCAAGCTTTTCAGGGCTTTGCCATGTGGCACTTTCATAGCAATGATATT 4614

Qy  
db

489 CATCGTATCCGAGACCTGGAGTTGTGTA TCGAGAAGATGCCCTTAGCAGC 544  
| | | | |  
4615 CTTCACTATGAGTCATTGTCATGCAGATGTTTGCAAGTGGCTTCTTCAGCAGC 4570  
| | | | |

RESULT 4  
A390175

**LOCUS** CA390175 593 bp mRNA linear EST 06-NOV-2002  
**DEFINITION** cs107d09.y1 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs107d09  
5' mRNA sequence

Accession  
CA390175  
Version  
CA390175.1 GI:24721013  
Keywords  
EST.  
Source  
Homo sapiens (human)

	Homo sapiens (human)	
	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
SEQUENCE	1-4768aa	

**REFERENCE**  
1. (pages 1 to 593)  
**AUTHORS**  
Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
**TITLE**  
Expressed sequence tag analysis of human RPE/choroid for the

JOURNAL  
MEDLINE  
22103460  
Mol. Vis. 8 (4), 205-220 (2002)  
splice variants  
and non-redundant transcripts, novel genes  
NEBank Project: Over 6000

12107410  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: [graeme@helix.nih.gov](mailto:graeme@helix.nih.gov)

Plate: 107 row: d column: 09  
Seq primer: M13rpi reverse primer (ABI).  
Location/Qualifiers  
source 1..593

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/Un-normalized="yes"
/Source="POMSPORT6: Two different donor
eyes (75-80 years old) isolated and
dissected RE/choroid tissue. This in turn yielded 340
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the POMSPORT6 vector was constructed at Life
Technologies, Gaithersburg, MD; now part of Invitrogen Corp.,
Carlsbad, CA. The library consists of the Superscript
Plasmid System (Invitrogen Corp.)
<http://www.invitrogen.com/>. The library code
designation was cs. For this library, cDNA inserts were
inserted into the NotI/Mut sites of the vector. EST
accession number is U05492. The unamplified library at the
NIH Intramural Sequencing Center is designated CH170838g

```

## ORIGIN

Query Match 2.3%; Score 40.6; DB 6; Length 593;  
Best Local Similarity 50.8%; Pred. No. 4.5;  
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0.

Qy	60	GGAGGAAGCAAGCTGCCATCAACGGCTGAGCAACTCCTTGCTGGTCACCATACCT	119
Dh	12	GTACAAACAAGGGTGGCATGAATCGGGAGACTGCTTCTCTCTCCGACGACATCTCT	71

QY 120 GGTCTATTCCACAACATCCGGCAGTGCAGCTGGCGAGAGAAGGTCACTTTGACAG 179

DB 72 CTCTCCACACAGCAATAGCGACAGTACACATTTCTGTCTCATCTACAGCATATGCGACCT 123

[illegible]

QY 240 CACAGTGAAGG 250  
| | | | |  
DB 192 CAGAGTGAAGG 202

20 122 INTERNATIONAL 202

RESULT 5  
00402500  
00402500

CN423579  
 LOCUS 665 bp mRNA linear EST 16-MAY-2004  
 DEFINITION 17000531603590 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
 ACCESSION CN423579

VERSION	CN423579.1	GI:47411173
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 665)  
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.  
 AUTHORS

**TITLE**  
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

**JOURNAL  
COMMENT**

230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: [vbrander@veritas.com](mailto:vbrander@veritas.com)

```

FEATURES
source
1. .665
Location/Qualifiers
Insert Length: 665 Std Error: 0.00.
Source: 1b1andmeger@eaton.com

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/tissue\_type="human"  
/dev stage="embryonic, 14.8 and 15.8 weeks (determined by foot length)"  
/clone\_lib="hxi; (MZPD no. 800)"  
Note: Vector: pGEMT (AF04176), site\_1: SalI; site 2: NotI. The library was prepared from mRNA obtained from brain material of two fet. 14.8 and 15.8 weeks old, with a Not I - oligo(dT) primer [5', 3' and 15.8 weeks old, with GACTGTCAGTACGTCGAGCGCGCCGCTTTTTTTTTTTT 3'].  
A cDNA library was ligated to Sal I adaptors and digested with NotI. The library was then stored in Sal I sites of the pGEMT vector. This cDNA expressed in E. coli library represents a subset of clones that were selected for protein expression and has been normalised by subtractive hybridisation and screening. The library was constructed by Kontor Biosoftware.

Query Match 2.24; Score 39; DB 6; Length 685;  
Best Local Similarity 47.41; Pred. No. 15;  
Matches 117; Conservative 0; Mismatches 130; Indels 0; Gaps 0;  
QY 37 GCCTGATACACATCGCTCGCTGCGAGGAGAGAGCTCCCATCAAGCGCTGAGCAAC 96  
Db 36 CGCGGCTCTACGAGGTTGGAGAGAGAGAGCGCGCGCGAGCGAGCGAGCAAC 95  
QY 97 TCTCTGCTGCTGACATACCTGGTCTATTCAACATATCGGACGTCAGCTGGCG 156  
Db 96 CTCCTGCTGCTGACATACCTGGTCTATTCAACATATCGGACGTCAGCTGGCG 155  
QY 157 CAGAGAGATGACGAGCGAGCGCTCCAGATGCTGAGAGATGCTGAGAGCGCTGC 216  
Db 156 AAGTGTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 215  
QY 217 AAGGAGATGAGCGAGCGAGCGCTCCAGATGCTGAGAGATGCTGAGAGCGCTGC 276  
Db 216 CGAGCTGCTGAGCGAGCGAGCGCTCCAGATGCTGAGAGATGCTGAGAGCGCTGC 275  
QY 277 TCGAGCG 283  
Db 276 GTGAGCG 282

RESULT 6  
LOCUS B0818891  
DEFINITION 602779275F2 NCI\_CGAP Brn67 Homo sapiens cDNA clone IMAGE:491481  
VERSION B0818891  
KEYWORDS B0818891.1 GI:14166478  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NRI-MGC <http://mgc.nci.nih.gov/>;  
JOURNAL The International Mouse Genome Consortium (MGC)  
COMMENT Unpublished (1999); Project: The International Mouse Genome Consortium (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: rstraub@fmail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
Library Construction: The MGC Technologies, Inc.  
CNA Library Arrived by The International Mouse Genome Consortium (ILMG)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/ILMG at: <http://www.imge.org>  
Plate: LAM10822 row: e column: 20  
High quality sequence stop: 783.  
Location/Qualifiers  
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/organism="Homo sapiens"

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FEATURES  
source

Location/Qualifiers

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/lab host="E. coli strain DH10B-T004"  
/note="Organ: Whole ticks and dissected organs; Vector:"

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Location/Qualifiers

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Seq primer: M3 reverse.

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Note: Vector: pGEMT (AF04176), site\_1: SalI; site 2: NotI. The library was prepared from mRNA obtained from brain material of two fet. 14.8 and 15.8 weeks old, with a Not I - oligo(dT) primer [5', 3' and 15.8 weeks old, with GACTGTCAGTACGTCGAGCGCGCCGCTTTTTTTTTTTT 3'].  
A cDNA library was ligated to Sal I adaptors and digested with NotI. The library was then stored in Sal I sites of the pGEMT vector. This cDNA expressed in E. coli library represents a subset of clones that were selected for protein expression and has been normalised by subtractive hybridisation and screening. The library was constructed by Kontor Biosoftware.

Query Match 2.24; Score 39; DB 4; Length 820;  
Best Local Similarity 47.41; Pred. No. 15;  
Matches 117; Conservative 0; Mismatches 130; Indels 0; Gaps 0;  
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QY 97 TCTCTGCTGCTGACATACCTGGTCTATTCAACATATCGGACGTCAGCTGGCG 156  
Db 157 CAGAGAGATGACGAGCGAGCGCTCCAGATGCTGAGAGATGCTGAGAGCGCTGC 216  
QY 217 AAGGAGATGAGCGAGCGAGCGCTCCAGATGCTGAGAGATGCTGAGAGCGCTGC 276  
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QY 277 TCGAGCG 283  
Db 251 GTGAGCG 257

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VERSION B0818891  
KEYWORDS B0818891.1 GI:14166478  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NRI-MGC <http://mgc.nci.nih.gov/>;  
JOURNAL The International Mouse Genome Consortium (MGC)  
COMMENT Unpublished (1999); Project: The International Mouse Genome Consortium (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: rstraub@fmail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
Library Construction: The MGC Technologies, Inc.  
CNA Library Arrived by The International Mouse Genome Consortium (ILMG)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/ILMG at: <http://www.imge.org>  
Plate: LAM10822 row: e column: 20  
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REFERENCE  
AUTHORS Nene, V.; Quackenbush, J.; George, J., and Guerrero, I.  
JOURNAL The Institute for Genomic Research  
COMMENT An index of genes transcribed in the tick Boophilus microplus  
Unpublished (2004)  
Contact: Vishwanath Nene  
Parasite Genomics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Fax: 301-818-0206  
Email: nene@igir.org  
Seq primer: M3 reverse.

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/note="Organ: Whole ticks and dissected organs; Vector:"

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Seq primer: M3 reverse.

Location/Qualifiers

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Seq primer: M3 reverse.



College of Medicine); available through Life Technologies.	
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Dy	230 CGGCGCTGATGAGAGAGGTTGAGAGAGAGCGCGCAGCGAGAGACCGAGCAAC 289
Qy	97 TCTTCTGCGTGCACCAATCTGCTTTATTCACAGATTCGCGTGTGATCTGCG 156
Dy	290 CTGTGCTCTTCCCGACAGAGCTGGAAGTCCATCTCTGTCCTGCTGAATCAGAGCG 349
Qy	157 CAGAGAGCTCAGCTTTTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216
Dy	350 AGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
Qy	217 AAGAGAGTGAAGCGAGCGCTCCACAGTGAAGCTTAACATCTGTTGAAGAGACCA 276
Dy	410 CGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
Qy	277 TCGAAGC 283
Dy	470 GTGAAGC 476
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ACCESSION	B0720548.1
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SOURCE	Homo sapiens (human)
ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 941)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
Version	Version
Keywords	Keywords
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Result 13	
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VERSION	B0673878
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KEYWORDS	EST.
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ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 954)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
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VERSION	B0673878
ACCESSION	B0673878.1 GI:21784724
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 954)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
Version	Version
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Organism	Organism
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VERSION	B0673878
ACCESSION	B0673878.1 GI:21784724
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 954)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
Version	Version
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KEYWORDS	EST.
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ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 954)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
Version	Version
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REFERENCE	1 (bases 1 to 954)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
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REFERENCE	1 (bases 1 to 954)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1995)
Accession	Accession
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VERSION	B0673878
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ORGANISM Homo sapiens (human)
REFERENCE Nakayama; Nakazawa; Chordara; Czanietz; Vercabrato; Bucleonemi;
AUTHORS 1 (bases 1 to 993)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1995)Steinberg, Ph.D.
Email: cagabn-remail.nih.gov
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Db	599	CGAGACTCTGAGGTGATGTGTGAGAGCGACAGGTGCGAGGTGAGGTGAGGCG	658
Oy	277	TGCAAGC	283
Db	659	GTGAAGC	665

Search completed: October 3, 2005, 22:17:01  
Job time : 5936.06 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 09:20:55 ; Search time 959.627 Seconds  
(without alignments)  
10733.697 Million cell updates/sec

Title: US-10-712-479-3

Perfect score: 1740

Sequence: 1 AGGTCATGAGCAGTC.....GCATCATCCATCATCATC 1740

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01  
Maximum Match 1001  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseq1980e:\*
- 2: Geneseq1990e:\*
- 3: Geneseq2000e:\*
- 4: Geneseq2001e:\*
- 5: Geneseq2001b:\*
- 6: Geneseq2002a:\*
- 7: Geneseq2002b:\*
- 8: Geneseq2002c:\*
- 9: Geneseq2003a:\*
- 10: Geneseq2003c:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004as:\*
- 13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SNMPARES

Result No.	Score	Query Match	Length	DB ID	Description
1	1740	100.0	1740	12	AD019022
2	1722	99.0	1803	12	AD019020
3	1555.6	89.4	1894	6	ADG19089 HCV NS5B
4	1551.8	89.2	9413	12	ADG24256 Hepatitis
5	1551.8	89.2	9413	12	ADG24256 Hepatitis
6	1551.8	89.2	9472	2	ADG37282
7	1547	88.9	7979	10	ADG93729 Hepatitis
8	1547	88.9	7979	10	ADG93730 Hepatitis
9	1547	88.9	7979	10	ADG93732 Hepatitis
10	1547	88.9	7979	10	ADG93732 Hepatitis
11	1547	88.9	9595	2	AAK24843
12	1547	88.9	9595	4	AAK23492
13	1547	88.9	9595	4	AAK86939
14	1547	88.9	9595	12	ADG93732 Hepatitis
15	1547	88.9	9595	12	ADG93732 Hepatitis
16	1545.4	88.8	7989	10	ADG93733 HCV
17	1543.8	88.7	9595	8	ACN61114 HCV cDNA
18	1543.8	88.7	9597	13	ADG82189 Hepatitis
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20	1540.4	88.5	1776	10	AA153597 DNA encod
					AA153596 DNA encod

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24	1538	88.4	9416	2	AAK59394
25	1537.4	88.4	9565	8	ACN61111
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28	1537	88.3	1779	2	AAK23195
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30	1535.6	88.3	9436	2	AA153599
31	1535.6	88.2	9436	2	AA153599
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34	1534.4	88.2	1779	2	AAK23199
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36	1534.2	88.2	3123	12	ADG93102
37	1535.9	88.0	1779	2	AAK23198
38	1527.8	87.8	7141	6	AAK25333
39	1527.8	87.8	7789	6	AAK25330
40	1527.8	87.8	7848	6	AAK25333
41	1527.8	87.8	7848	6	AAK25333
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# ALIGNMENTS

## RESULT 1

## AD019022

ID AD019022 standard; DNA; 1740 BP.

XX AD019022;

DT 12-AUG-2004 (first entry)

DE DNA encoding C-terminally truncated HCV NS5B polymerase, Cdelta21 NS5B.

XX RNA polymerase activity; continuous read assay;

XX Hepatitis C virus infection; HCV infection; polymerase, NS5B;

XX bone mineral disease; osteoporosis; carcinoma; cardiovascular disease;

XX diabetes; ocular disorder; renal dysfunction; lymphoma;

XX sleep disorder; metabolic disorder; arthritis;

XX viral disease; hepatitis; hepatitis; hepatitis; hepatitis;

XX viraemia; osteopathic; cytotoxic; antidiabetic; ophthalmological;

XX nephrotropic; antihypertensive; gene; da.

XX Hepatitis C virus.

Key Location/Qualifiers

FT CDS

1..1740

/\*tag=a

/product="Cdelta21 NS5B"

/note="This sequence lacks a stop codon"

XX

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XX







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 Db 1141 TCTGGCAAAAGGGTGTTACTACTACCTACCCGACCTCCGCTCCGCTTGGCGGGCTGG 1200  
 QY 1201 TGGGAGGACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
 Db 1201 TGGGAGGACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
 QY 1261 CCGACCTTTGTGGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
 Db 1261 CCGACCTTTGTGGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
 QY 1321 GAGCACTGTGAAAAGCCCTGGATGTGTGAGATCTAGCGGGCTGTGTACTCAATGAGCCA 1380  
 Db 1321 GAGCACTGTGAAAAGCCCTGGATGTGTGAGATCTAGCGGGCTGTGTACTCAATGAGCCA 1380  
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 Db 1381 CTGAGACTTACTGAGATCACTGAGGAGCACTCATGCTTTAGGGGATTTTCACTCATGAT 1440  
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 QY 1501 TGGCACTCTGAGAGCAGTGGGCGAGAGTGTGCGGCTGAAGTACTGCTTCCGAGGGGGG 1560  
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 Db 1681 GGGGAGGAGATATATGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1722

## RESULT 3

ADG19089  
 XX ADG19089 standard; DNA; 1884 BP.  
 AC ADG19089;  
 XX 26-FEB-2004 (first entry)  
 DE HCV NS5B polymerase coding sequence, SEQ ID 11.  
 XX  
 KW Virucide; initiation site; RNA polymerase; RdRp; polypyrimidine tract;  
 XX HCV; NS5B RNA-dependent RNA polymerase, gene, db.  
 OS Hepatitis C virus.

Key Location/Qualifiers  
 FH /tag a  
 CD5 /product= "HCV NS5B polymerase"  
 FT  
 FT  
 XX MO200183736-A2.

08-NOV-2001.

20-APR-2001; 2001MO-CA00580.

21-APR-2000; 2000US-0198733P.

XX (BOEH) BOEHRINGER INGELHEIM CANADA LTD.

XX Pellerin C, Kukolj G;

XX

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XX

DR MP1; 2002-066531/09.  
 XX P-RD8; ADG19078.  
 XX Internal de novo initiation site of RNA-dependent RNA polymerase which  
 XX provides a RNA template for assessing polymerase activity, has  
 PT polypyrimidine tract having a cytidylate nucleotide located in it or  
 PT adjacent to it.  
 XX  
 XX Example 1; Page 45-46; 49pp, English.  
 XX  
 CC The present invention relates to isolated de novo initiation sites (1;  
 CC ADG19099-ADG19102) for an RNA-dependent RNA polymerase (RdRp) set two or  
 CC consist essentially of polyuracil residues located in it or  
 CC adjacent to it. The RdRp is the Hepatitis C virus (HCV) NS5B RNA-  
 CC dependent RNA polymerase, its analog, variant or derivative. Also claimed  
 CC are (1) templates (II) for primer-independent RNA synthesis  
 CC comprising a) and b) and c) and d) and e) and f) and g) and h) and i) and j) and k) and l) and m) and n) and o) and p) and q) and r) and s) and t) and u) and v) and w) and x) and y) and z) and aa) and ab) and ac) and ad) and ae) and af) and ag) and ah) and ai) and aj) and ak) and al) and am) and an) and ao) and ap) and aq) and ar) and as) and at) and au) and av) and aw) and ax) and ay) and az) and ba) and bb) and bc) and bd) and be) and bf) and bg) and bh) and bi) and bj) and bk) and bl) and bm) and bn) and bo) and bp) and bq) and br) and bs) and bt) and bu) and bv) and bw) and bx) and by) and bz) and ca) and cb) and cc) and cd) and ce) and cf) and cg) and ch) and ci) and cj) and ck) and cl) and cm) and cn) and co) and cp) and cq) and cr) and cs) and ct) and cu) and cv) and cw) and cx) and cy) and cz) and da) and db) and dc) and dd) and de) and df) and dg) and dh) and di) and dj) and dk) and dl) and dm) and dn) and do) and dp) and dq) and dr) and ds) and dt) and du) and dv) and dw) and dx) and dy) and dz) and ea) and eb) and ec) and ed) and ee) and ef) and eg) and eh) and ei) and ej) and ek) and el) and em) and en) and eo) and ep) and eq) and er) and es) and et) and eu) and ev) and ew) and ex) and ey) and ez) and fa) and fb) and fc) and fd) and fe) and ff) and fg) and fh) and fi) and fj) and fk) and fl) and fm) and fn) and fo) and fp) and fq) and fr) and fs) and ft) and fu) and fv) and fw) and fx) and fy) and fz) and ga) and gb) and gc) and gd) and ge) and gf) and gg) and gh) and gi) and gj) and gk) and gl) and gm) and gn) and go) and gp) and gq) and gr) and gs) and gt) and gu) and gv) and gw) and gx) and gy) and gz) and ha) and hb) and hc) and hd) and he) and hf) and hg) and hh) and hi) and hj) and hk) and hl) and hm) and hn) and ho) and hp) and hq) and hr) and hs) and ht) and hu) and hv) and hw) and hx) and hy) and hz) and ia) and ib) and ic) and id) and ie) and if) and ig) and ih) and ii) and ij) and ik) and il) and im) and in) and io) and ip) and iq) and ir) 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 QY 128 CACACACATCCCGCAGTGCAGCTTGGGGCAGAGAGGTGTCACCTTTGACAGACTCGAAG 187  
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 QY 188 TCTGTGAGCATCATACCGGACATGCTTCAGGCGAGAGGCGGCTCCACAGTGA 247  
 Db 284 TCTGTGAGCATCATACCGGACATGCTTCAGGCGAGAGGCGGCTCCACAGTGA 343  
 QY 248 AGGCTTAACCTGTTTCTGTGAGAGAGCATCAAGCTGAGGCGCGCGGCGGATCGGCGCAAT 307  
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 QY 308 CCAAAATTGCTATGCGGCAAGGACCTGCGGCGGCTTCGACAGCGCGCGGTACACCA 367  
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967	CTGCTGAGCTGATGATGATCTGGGCTCCGACGACGACGACGACGACGACGACGACG 967	
1004	CTGCTGAGCTGATGATGATCTGGGCTCCGACGACGACGACGACGACGACGACGACG 1063	
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1508	TCTGGAGCATGATGATGATGATCTGGGCTCCGACGACGACGACGACGACGACGACGACG 1567	
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[illegible]

















GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 14:01:52 ; Search time 1226.79 Seconds  
(without alignments)  
9793.114 Million cells updates/sec

Title: US-10-712-479-3

Perfect score: 1740  
Sequence: 1 aggtcctacgcacatgc.....gcattccaccatccatcac 1740

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs. 3452328358 residues

Total number of hits at selected chosen parameters: 14895122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 01

Listing first 45 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best matching printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1740	99.0	0	US-10-712-479-3	Sequence 3, Appli
2	1722	99.0	180	20 US-10-712-479-3	Sequence 1, Appli
3	1555	89.4	1884	9 US-09-838-386-11	Sequence 1, Appli
4	1543	88.7	5955	20 US-10-492-178-5	Sequence 5, Appli
5	1537	88.4	5965	20 US-10-492-178-2	Sequence 2, Appli
6	1537	88.4	5965	20 US-10-492-178-4	Sequence 4, Appli
7	1527	87.8	6189	15 US-10-439-275-41	Sequence 41, Appli

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8 1527.8 87.8 6189 24 US-11-006-313-41 Sequence 41, Appli
9 1527.8 87.8 6189 24 US-10-434-842-16 Sequence 16, Appli
10 1527.8 87.8 7989 21 US-10-897-648-17 Sequence 1, Appli
11 1527.8 87.8 7989 21 US-10-897-648-17 Sequence 1, Appli
12 1527.8 87.8 7992 13 US-10-005-469-11 Sequence 1, Appli
13 1527.8 87.8 7992 13 US-10-005-469-11 Sequence 2, Appli
14 1527.8 87.8 7992 13 US-10-005-469-11 Sequence 3, Appli
15 1527.8 87.8 7992 13 US-10-005-469-11 Sequence 4, Appli
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21 1527.8 87.8 7992 17 US-10-434-842-1 Sequence 4, Appli
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32 1527.8 87.8 1772 19 US-10-384-339C-132 Sequence 132, App
33 1527.8 87.8 8638 17 US-10-434-842-17 Sequence 17, Appli
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36 1526.2 87.7 8638 13 US-10-029-907-24 Sequence 24, Appli
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38 1526.2 87.7 8638 15 US-10-309-561-9 Sequence 6, Appli
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40 1526.2 87.7 8638 15 US-10-309-561-9 Sequence 24, Appli
41 1526.2 87.7 8638 15 US-10-309-561-24 Sequence 24, Appli
42 1526.2 87.7 8638 15 US-10-309-561-25 Sequence 25, Appli
43 1526.2 87.7 8638 19 US-10-789-358-6 Sequence 6, Appli
44 1526.2 87.7 8638 19 US-10-789-358-6 Sequence 7, Appli
45 1526.2 87.7 8638 19 US-10-789-355-24 Sequence 4, Appli
46 1526.2 87.7 8638 19 US-10-789-355-24 Sequence 5, Appli
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#### ALIGNMENTS

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RESULT 1 12-479-3
US-10-712-479-3
Sequence 3, Application US/10712479
Publication No. US2004020293A1
GENERAL INFORMATION:
APPLICANT: Yael, Yoshiko
INVENTOR: Shelly, Joan A.
APPLICANT: Shelly, Joan A.
APPLICANT: Poorman, Roger A.
APPLICANT: Epps, Dennis E.
TITLES OF INVENTION: Continuous-Read Assay for the Detection of De Novo HCV RNA Poly
ACTIVITY
CURRENT APPLICATION NUMBER: US/10712.479
CURRENT FILING DATE: 2003-11-13
NUMBER OF CLAIMS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1740
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#### FEATURES

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OTHER INFORMATION: C-terminally truncated HCV NS5B polymerase (C delta 21 NS5B)
FEATURE:
LOCATION: CDS
LOCATION: (1) ..(1740)
OTHER INFORMATION:
US-10-712-479-3
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## OTHER INFORMATION:

US-10-712-479-1

Query Match 99.0%; Score 1722; DB 20; Length 1803;

Similarity 100.0%; Pred. No. 0;

Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GAGGAGACAGCTGCCCATGAGCGCGTACGACCTCTGCTGCTCAGCATACCTG 120  
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Qy 121 GCTATTATCAACAGCTGAGCTGAGCTGCGGACGAGAGAGTCACTTTCAGAG 180  
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Qy 181 CTCGACAGTCTGAGAGATATATACCGGAGCTGCTGACAGAGATGAGAGCGG 240  
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Qy 241 ACAGTAGAGCTGATATACCGGAGCTGCTGACAGAGATGAGAGCGGAGCGG 300  
 Db 241 ACAGTAGAGCTGATATACCGGAGCTGCTGACAGAGATGAGAGCGGAGCGG 300

Qy 301 GCCAATTCOAATTTGCTATGCGGCAAGAGCTCCGAGCTATACGAGAGGCGTT 360  
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Qy 361 AACCATACGCTCGGTGTGAGAGGACTTCTGAGAGCACTGACACCAATTCAGACC 420  
 Db 361 AACCATACGCTCGGTGTGAGAGGACTTCTGAGAGCACTGACACCAATTCAGACC 420

Qy 421 ACCATCATGTCGCAAAAATGAGGTTTTCTGCTGACACAGAGAGAGCGCGCAACCA 480  
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Qy 481 GCTGCGCTCATGCTATTCAGAGCTGGAGGTCGCTGATATGAGAGATGAGCTTTAC 540  
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Qy 601 CTTCAGAGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
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Qy 721 GAGTCATATTAACAGCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
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Qy 841 CGCGGCTGCT 900  
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Qy 901 TTGAGAGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCT 960  
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Qy 1681 GGGGAGACATATATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1722  
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## RESULT 3

US-09-838-386-11  
 ; Sequence ID: US-09-838-386-11  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pellerin, Charles  
 ; APPLICANT: Kukuji, George  
 ; TITLE OF INVENTION: Internal  
 ; FILE REFERENCE: 1011.218001  
 ; CURRENT APPLICATION NUMBER: US/09/838.386  
 ; CURRENT FILING DATE: 2001-04-20  
 ; PRIORITY FILING DATE: 2001-04-21  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 11  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature

US-10-712-479-1

OTHER INFORMATION: HTAASB polymerase

NAME/KEY: CDS

LOCATION: (1).. (1881)

US-09-838-386-11

Query Match 89.4%; Score 1555.6; DB 9; Length 1884;

Best Local Similarity 94.2%; Pred. No. 0;

Matches 1615; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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128 CGGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCT 187

224 CGGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCT 283

188 TCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCT 247

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248 GATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCTGATGAGTCT 307

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US-10-492-178-5

Application US/10492178

Publication No. US20040247615A1

GENERAL INFORMATION:

APPLICANT: Bains, Emilio A.

APPLICANT: Bains, Andrew J. C.

APPLICANT: Shives, John W.

APPLICANT: Shives, John W.

APPLICANT: Lohm, Richard

APPLICANT: Lohm, Alessandra

APPLICANT: Cortese, Riccardo

APPLICANT: Colloca, Stefano

TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE

CURRENT APPLICATION NUMBER: US/10492178

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: PCT/US02/33512

PRIOR FILING DATE: 2002-10-10

RESULT 4

US-10-492-178-5

Application US/10492178

Publication No. US20040247615A1

GENERAL INFORMATION:

APPLICANT: Bains, Emilio A.

APPLICANT: Bains, Andrew J. C.

APPLICANT: Shives, John W.

APPLICANT: Shives, John W.

APPLICANT: Lohm, Richard

APPLICANT: Lohm, Alessandra

APPLICANT: Cortese, Riccardo

APPLICANT: Colloca, Stefano

TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE

CURRENT APPLICATION NUMBER: US/10492178

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: PCT/US02/33512

PRIOR FILING DATE: 2002-10-10

[illegible]





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RESULT 6
US-10-492-178-4
  FILE REFERENCE: ITR0015VP
  PUBLICATION NO. US20040247615A1
  GENERAL INFORMATION:
    APPLICANT: Eniri, Emilio A.
    APPLICANT: Rieton, David C.
    APPLICANT: Shiver, John W.
    APPLICANT: Nicosia, Alfredo
    APPLICANT: Latm, Amin
    APPLICANT: Coraggio, Alessandra
    APPLICANT: Collica, Stefano
  TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
  FILE REFERENCE: ITR0015VP
  CURRENT FILING DATE: 2004-04-07
  PRIOR APPLICATION NUMBER: US/10/492,178
  PRIOR FILING DATE: 2002-10-10
  PRIOR APPLICATION NUMBER: PCT/US02/32512
  PRIOR FILING DATE: 2002-10-10
  PRIOR APPLICATION NUMBER: 60/363,774
  PRIOR FILING DATE: 2001-10-11
  PRIOR APPLICATION NUMBER: 60/328,655
  NUMBER OF SEQ ID NOS: 17
  SOURCE: PAKSHO FOR Windows Version 4.0
  SEQ ID NO: 1
  LENGTH: 7090
  TYPE: DNA
  ORGANISM: Artificial Sequence
  OTHER INFORMATION: MKK4de-NSmuc nucleic acid
US-10-492-178-4

Query Match      88.4%; Score 1537.4; DB 20; Length 7090;
Res Local Similarity 93.5%; Pred. No. 0;
Matches 160; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY      8  GATGTCAATGTCTTATACATGGACAGCGCCCTGATCAACAAGCTGCGCTGGACGAA 67
DB      5441  GCTGCTCTCATGTCCTACATCATGACAGAGAGGCTCTGATCAAGCATGCTGCTGGAGAAA 5500

QY      68  GAAAGCTGGCCCATCAAGCGCTGAGCAACTCTCTGGCTGACATACGCTGCTAT 127
DB      5501  GGAAGCTGGCCCATCAAGCGCTGAGCAACTCTCTGGCTGACATACGCTGCTAT 127

QY      128  CCAAGCATCCGACATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 5560
DB      5561  CCAAGCATCCGACATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 5620

QY      188  TCGTGGAGCATGTTACCGGAGCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 247
DB      5621  TCGTGGAGCATGTTACCGGAGCGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 247

QY      248  AGGCTAACTCTTATCTGTAGAGAGAGATGGAAGCTGAGCTGAGCTGAGCTGAGCT 307
DB      5681  AGGCTAACTCTTATCTGTAGAGAGAGATGGAAGCTGAGCTGAGCTGAGCTGAGCT 307

QY      308  CCAATATTCGATATGGGCAAGAGAGCTCCGAGAGCTATTCAGAGAGAGAGAGAG 367
DB      5741  CCAATATTCGATATGGGCAAGAGAGCTCCGAGAGCTATTCAGAGAGAGAGAGAG 367

QY      368  TCGCTCTCTGTGAGAGAGCTGCTGGAGAGAGCTGAGAGAGAGAGAGAGAGAGAG 427
DB      5801  TCGCTCTCTGTGAGAGAGCTGCTGGAGAGAGCTGAGAGAGAGAGAGAGAGAGAG 427

QY      428  TGGCAAAAATGAGGTTTCTGCTGCTCAACGAGAGAGAGAGAGAGAGAGAGAG 487
DB      5861  TGGCAAAAATGAGGTTTCTGCTGCTCAACGAGAGAGAGAGAGAGAGAGAGAG 487

QY      488  TCATGTATCTCCAGACCTGGAGATCTGTGTATTCGAGAGAGATGGCCCTTTA 547
DB      5921  TTAATCTCCAGACCTGGAGATCTGTGTATTCGAGAGAGATGGCCCTTTA 547

QY      548  TTTCATCTCTCTCGAGCGCTGATGGGCTCTCATAGGANTCCATACCTCTCTTAAG 607
DB      5981  TTTCATCTCTCTCGAGCGCTGATGGGCTCTCATAGGANTCCATACCTCTCTTAAG 607

QY      608  AGCGGGTGGAGTCTCTGTGATACCTGGAAGCAAGAGAAAGCGCCCTCTCTCT 667
DB      6041  AGCGGGTGGAGTCTCTGTGATACCTGGAAGCAAGAGAAAGCGCCCTCTCTCT 667

QY      668  ATGACACACCGCGGCTTCTGATCATAGCGCTCATGAGAGATCATGCTGTGTAGAG 727
DB      6101  ATGACACACCGCGGCTTCTGATCATAGCGCTCATGAGAGATCATGCTGTGTAGAG 727

QY      728  TTATACATATGTGTGATCTGCGCGGAGAGCTAGACAGGCTATAGCTGCTCTACAG 787
DB      6161  TTATACATATGTGTGATCTGCGCGGAGAGCTAGACAGGCTATAGCTGCTCTACAG 787

QY      788  GAGCTCTATGTGGGGGTCCATGATCTAACTCAAGAGGAGAGAACTGGGCTATGGCG 847
DB      6221  GAGCTCTATGTGGGGGTCCATGATCTAACTCAAGAGGAGAGAACTGGGCTATGGCG 847

QY      848  CGCGCGGAGCGGCTGCTGAGCAAGCTAGCTGCGCTATACCTCATGATGCTACTGAAG 907
DB      6281  CGCGCGGAGCGGCTGCTGAGCAAGCTAGCTGCGCTATACCTCATGATGCTACTGAAG 907

QY      908  CCGCTGACGAGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 967
DB      6341  CCGCTGACGAGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 967

QY      968  ACCTGTGCTTATCTGTGAAGAGCGGAGCAACCGAGAGAGAGAGAGAGAGAGAG 1027
DB      6461  ACCTGTGCTTATCTGTGAAGAGCGGAGCAACCGAGAGAGAGAGAGAGAGAGAG 1027

QY      1028  TACGAGAGAGCTATGATAGCTAGCTGCTGCGCGGCTGCGGAGCGCGAGAGAGAG 1087
DB      6461  TACGAGAGAGCTATGATAGCTAGCTGCTGCGCGGCTGCGGAGCGCGAGAGAGAG 1087

QY      1088  ACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
DB      6521  ACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147

QY      1148  AAAGGGGTACTTACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1207
DB      6581  AAAGGGGTACTTACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1207

QY      1208  CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1267
DB      6641  CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1267

QY      1268  TGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1327
DB      6701  TGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1327

QY      1328  TGTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1387
DB      6761  TGTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1387

QY      1388  TACCTCAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1447
DB      6821  TACCTCAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1447

QY      1448  CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1507
DB      6881  CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1507

QY      1508  TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567
DB      6941  TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567

QY      1568  CAAATTTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627
DB      6941  CAAATTTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627

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Db	7355	TACCTCAGATCATTCACAGATCTCCATGGCTTACGCCATTTTCCTCATGTACTCTC	7414
Qy	1448	CAGGTGATGATGATGATGGTGGCTTACATGCTCAGAGAGCTTGAGGTATCAACCTTGGAG	1507
Db	7415	CAAGTGGATCATGAGTGGCTTCATGCTCAAGAAATTCGGGTATACCGCTCTTGGAG	7474
Qy	1508	TCCTGAGACATCCGCGCAGAGATGTCGCGCTTAAGTATGCTCCAGGGGGGGGGAGCG	1567
Db	7475	TCCTGGAGGACAGAGTCCAGAGCTTACGCTACGCTATCTCCAGGGGGGGGGAGCTC	7534
Qy	1607	TCATTTGGTGGCAAGCTACTCTCACTGGGCGATGAGGACCAAGCTTAAACTCACTCCAA	1627
Db	7535	CGACTCTGTGGCAGATGATCTCTTCACTGGGGAGTGAAGCACACAGTCAAACTCTCAA	7594
Qy	1628	TTCCGCGCTGGCTCGCGCTGAGATCTGCGGCTGGCTGGCTGAGCTCAAGCGGAGAG	1687
Db	7595	TCCCTGCGCTGGCTCGCGCTGAGATCTGAGTATATCAAGATGGTGTGCTGCTAGCAGCGGAGAG	7654
Qy	1688	TAAGATATATCATCAAGCTGTCTGGTGGCGAGCAACCGCCG	1722
Db	7655	ACATATATATCATCAAGCTGTCTGGTGGCGAGCAACCGCCG	7689















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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: October 3, 2005, 13:25:15 | Search time 298.103 Seconds  
9550.788 Million cell updates/sec

Title: US-10-712-479-3

Perfect score: 1740  
Sequence: 1 atgcgttagcagcgaagc.....gcatcaccaccaccatcac 1740

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 120784 seqs, 811138359 residues

Total number of hits satisfying chosen parameters: 2405560

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /cgn2\_6/pcodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/pcodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/pcodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/pcodata/1/ina/6C\_COMB.seq.\*  
6: /cgn2\_6/pcodata/1/ina/backlitest.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score of 1740 or greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1551.8	89.2	9472	4	US-08-150-2048-96
2	1537.7	88.9	9595	3	US-09-014-416-4
3	1536.6	88.5	2991	2	US-08-384-616-49
4	1535.6	88.5	2991	2	US-08-384-616-49
5	1535.6	88.5	2991	2	US-08-384-616-49
6	1535.6	88.5	2991	3	US-08-315-850-49
7	1535.6	88.5	7863	3	US-08-324-977-35
8	1535.6	88.5	7863	3	US-08-324-977-35
9	1535.6	88.5	7863	3	US-08-304-686A-35
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13	1535.6	88.5	7917	3	US-09-115-850-31
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15	1535.6	88.5	9030	1	US-08-324-977-13
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18	1535.6	88.5	9030	3	US-09-115-850-13
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20	1535.6	88.5	9416	2	US-08-384-616-1
21	1535.6	88.5	9416	2	US-08-384-616A-1
22	1535.6	88.5	9416	3	US-09-115-850A-1
23	1535.6	88.5	9416	3	US-09-115-850A-1
24	1537.8	87.8	7869	4	US-09-539-601-10
25	1527.8	87.8	8001	4	US-09-539-601-7
26	1527.8	87.8	8001	4	US-09-539-601-22
27	1527.8	87.8	8001	4	US-09-539-601-4
28	1527.8	87.8	8649	4	US-09-539-601-13
29	1527.8	87.8	11076	4	US-09-539-601-1
30	1527.8	87.8	11076	4	US-09-539-601-25
31	1526.2	87.7	8001	4	US-09-539-601-68
32	1526.2	87.7	8638	4	US-10-028-907-68
33	1526.2	87.7	8638	4	US-10-028-907-24
34	1526.2	87.7	8638	4	US-10-028-907-75
35	1526.2	87.7	8639	4	US-10-028-907-15
36	1526.2	87.7	8639	4	US-10-028-907-25
37	1526.2	87.7	8642	4	US-10-028-907-2
38	1526.2	87.7	11076	4	US-09-539-601-31
39	1526.2	87.7	8001	4	US-09-539-601-16
40	1524.6	87.6	8001	4	US-09-539-601-11
41	1524.6	87.6	8648	4	US-10-028-907-5
42	1524.6	87.6	11076	4	US-09-539-601-19
43	1523.6	87.6	9413	4	US-09-827-688-6
44	1523.6	87.5	1773	4	US-09-720-095A-1
45	1513.8	87.3	1782	3	US-09-597-877-11

#### RESULT 1

US-08-150-2048-96

Sequence 96, Application US/08150204R

Patent status: Pending

GENERAL INFORMATION:

APPLICANT: CHO, Joong Myung

LEE, Yong Beom

PARK, Young Woo

CHOI, Deog Young

SO, Hong Seob

KIM, Chun Hyung

KIM, Sung Taek

YANG, Jae Young

STREET: 166, Doryong-dong, Yuseong-gu

CITY: Daejeon

STATE: Daejeon

COUNTRY: Republic of Korea

COMPUTER RELEVABLE FORM:

MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage

COMPUTER: IBM PC/pentium

OPERATING SYSTEM: Windows

FILE NAME: US-08-150-2048-96

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/150,204E

FILING DATE: 20-Apr-1994

CLASSIFICATION: <Unknown>

PRIOR:

APPLICATION NUMBER: KR 91-9510

FILING DATE: 10-JUN-1991

APPLICATION NUMBER: KR 91-13601

ATTORNEY: Shahan Telan

NAME: Shahan Telan

REGISTRATION NUMBER: 32,507

REFERENCE/DOCKET NUMBER: 2695/FLX

TELEPHONE: (212) 940-8776

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TELEPHONE: (212) 940-8776

#### ALIGNMENTS

Sequence 13, Appl  
Sequence 1, Appl  
Sequence 25, Appl  
Sequence 28, Appl  
Sequence 7, Appl  
Sequence 24, Appl  
Sequence 25, Appl  
Sequence 3, Appl  
Sequence 31, Appl  
Sequence 16, Appl  
Sequence 4, Appl  
Sequence 19, Appl  
Sequence 6, Appl  
Sequence 1, Appl  
Sequence 11, Appl

MOLECULE TYPE: DNA

FEATURES:

OTHER INFORMATION: KICV-LBCL1, FIG. 2

SEQUENCE DESCRIPTION: SEQ ID NO: 96

US-08-150-204E-96

Query Match 69.2%; Score 1551.8; DB 4; Length 9472;

Best Local Similarity 94.1%; Pred. No. 0;

Matches 1613; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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7595 AGCTGTGATGCTCTACATGACGAGCGCGCTGATCAACCCGCTGCGCGAGGAA 7654

68 GCACTCAAGAGCTCTATACATGACGAGCGCTGATCAACCCGCTGCGCGAGGAA 127

7655 GCACTGTGATGCTCTACATGACGAGCGCGCTGATCAACCCGCTGCGCGAGGAA 7714

128 CCAACATTCGCGATGCGAGCTCTGCGAGCGCTGATCAACCCGCTGCGCGAGGAA 387

7715 CTCAACATTCGCGATGCGAGCTCTGCGAGCGCTGATCAACCCGCTGCGCGAGGAA 7774

188 TCTTGGACGATCATACGCGAGCTCTGCGAGCGCTGATCAACCCGCTGCGCGAGGAA 247

7775 TCTTGGACGATCATACGCGAGCTCTGCGAGCGCTGATCAACCCGCTGCGCGAGGAA 7834

248 AGCTTAACCTCTATCTGAGAGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 307

7835 AGCTTAACCTCTATCTGAGAGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 7894

308 CCAAAATTCGGTATGCGGAGAGAGCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 367

7895 CCAAAATTCGGTATGCGGAGAGAGCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 7954

368 TCGCTGCTGCTGAGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 427

7955 TCGCTGCTGCTGAGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 8014

428 TCGCAAAATTCGGTATGCGGAGAGAGCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 487

8015 TCGCAAAATTCGGTATGCGGAGAGAGCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 8074

488 TCAATGATATCCAGATCTGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 547

8075 TCAATGATATCCAGATCTGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 8134

548 TTTCACTCTCTCTACGCGCTGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 607

8135 TTTCACTCTCTCTACGCGCTGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 8194

608 AGCGGCTGAGCTCTCTACGCGCTGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 667

8195 AGCGGCTGAGCTCTCTACGCGCTGAGAGCTCTGCGAGCGCTTCCAGAGCGCGCTTAAACACA 8254

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8255 ATGACAGCCGCTGCTTTGAGCTCAACGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 8314

728 TTACACAAATTCGCTTTGAGCTCAACGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 787

8315 TTACACAAATTCGCTTTGAGCTCAACGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 8374

788 GCGCTGCTGCTGCGGCTGCTGAGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 847

8375 GCGCTGCTGCTGCGGCTGCTGAGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 8434

848 GCGCTGCTGCTGCGGCTGCTGAGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 907

8495 GCGCTGCTGCTGCGGCTGCTGAGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 8949

908 CCGCTGCTGCTGCGGCTGCTGAGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 967

8495 CCGCTGCTGCTGCGGCTGCTGAGCTCACTGAGATGAGATCTGCTGAGAGCGGAA 8554

968 ACTTGTGTTATCTGTAAGAGCGGGAACCCCAAGAGACGCGCAAGCTTCAAGATCT 1027

8545 ACTTGTGTTATCTGTAAGAGCGGGAACCCCAAGAGACGCGCAAGCTTCAAGATCT 8614

1028 TCAAGAGCTATGATAGGTACTCTGCCCCCCCCCGGAGACCGCCCAACGAGATACG 1087

8615 TCAAGAGCTATGATAGGTACTCTGCCCCCCCCCGGAGACCGCCCAACGAGATACG 8674

1147 ACTTGAGCTGATACATGCTGCTCTCAATGTGTGCTGCGCAACGATGATCTGCA 1147

8734 ACTTGAGCTGATACATGCTGCTCTCAATGTGTGCTGCGCAACGATGATCTGCA 8734

1148 AAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1207

8735 AAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8734

1208 CAGCTAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1267

8854 CAGCTAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8854

1327 TGTGCGAAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1327

8914 TGTGCGAAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8914

1328 TGAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1387

8915 TGAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8914

1447 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1447

9034 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9034

1448 CAGCTGAGATCAATGAGGTGCTGATGCTTCAAGAGCTTGGGCTACACCCCTTGGAG 1507

9094 CAGCTGAGATCAATGAGGTGCTGATGCTTCAAGAGCTTGGGCTACACCCCTTGGAG 9094

1507 TCTGAGACATCGGCTGAGAGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1567

9154 TCTGAGACATCGGCTGAGAGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 9154

1627 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1627

9214 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9214

1628 TTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1687

9215 TTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9215

1688 ACATATATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1722

9275 ACATATATACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9309

RESULT 2

US-09-014-416-4

Patent No. 6,153,421

GENERAL INFORMATION:

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

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APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

APPLICANT: Yanagi, Masayuki

```

; LENGTH: 9595
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-014-416-4

Query Match
Best Local Similarity 93.94; Pred. No. 0;
Matches 1610; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY      8  GCATGTCATGCTCTATACATGACGAGCGCCCTGATCAACAGCTGCGCGCGGAGAA 67
Db      7594  GCCTCATGCTCTCTATAGCTGACAGCGCCCTGATCAACGCTCATGCTGCGAGGAA 7653

QY      68  GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 127
Db      7654  GTTAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12713

QY      128  CGACACATCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 187
Db      7714  CCACAGATGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7773

QY      188  TCGTGGAGCATATTACCGGAGCGCTGCTCAAGGAGTGAAGGAGAGCGGCTCCACG 247
Db      7774  TCGTGGAGCATATTACCGGAGCGCTGCTCAAGGAGTGAAGGAGAGCGGCTCCACG 7833

QY      248  AGCTTAAATCTGATCTGTAGAGAGAGATGCAAGCTTCAAGCGCCCGATGATGCG 307
Db      7834  AGCTTAAATCTGATCTGTAGAGAGAGATGCAAGCTTCAAGCGCCCGATGATGCG 7893

QY      308  CCAATTTTGGCTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db      7894  CCAATTTTGGCTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7953

QY      368  TCGCTGCTGCTGCGAGAGCTCTGCTGGAGCACTGACACACACACACACACACAC 427
Db      7954  TCGCTGCTGCTGCGAGAGCTCTGCTGGAGCACTGACACACACACACACACACAC 8013

QY      428  TCGCGAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 487
Db      8014  TCGCGAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8073

QY      488  TATGATGATCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db      8074  TATGATGATCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8133

QY      548  TTCTCATCTCTCTCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 607
Db      8134  TTCTCATCTCTCTCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8193

QY      608  AGCGGCTGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
Db      8194  AGCGGCTGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6733

QY      668  ATGACGACCGCGCTTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
Db      8254  ATGACGACCGCGCTTTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8313

QY      728  TTATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
Db      8314  TTATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8373

QY      788  GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
Db      8374  GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8433

QY      848  CGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
Db      8434  CGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8493

QY      908  CCGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
Db      8494  CCGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9553

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# Sequence 3

US-08-324-977-49

; Sequence 49; Application US/08324977

; Patent No. 5747339

; GENERAL INFORMATION:

; APPLICANT: HATTORI, Hattori, McLeod &

; APPLICANT: MORI, Chisato

; APPLICANT: MORI, Chisato

; APPLICANT: TAKAMIZAWA, Akahisa

; APPLICANT: YOSHIDA, Iwao

; APPLICANT: YOSHIDA, Iwao

; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESS: Amstrong, Hattori, McLeod &

; STREET: 1725 Washington

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

```

QY      968  ACCTTGCTTATCTGTGAAGCGCGCGGAACTCCAGAGGAGCGCGGACGCTTAGCTCT 1027
Db      9554  ACCTTGCTTATCTGTGAAGCGCGCGGAACTCCAGAGGAGCGCGGACGCTTAGCTCT 10613

QY      1028  TCACGAGAGCTATGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1887
Db      8614  TCACGAGAGCTATGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8673

QY      1088  ACCTTGAGAGCTATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1147
Db      8674  ACCTTGAGAGCTATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8733

QY      1148  AAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207
Db      8734  AAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8793

QY      1208  CAGCTTAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267
Db      8794  CAGCTTAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8853

QY      1268  TGTGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327
Db      8854  TGTGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8913

QY      1328  TTGAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1387
Db      8914  TTGAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8973

QY      1388  TACTCTGAGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
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QY      1448  CAGGTGAGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1507
Db      9034  CAGGTGAGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9093

QY      1508  TCTGAGAGATGCGGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1567
Db      9094  TCTGAGAGATGCGGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9153

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/315,850
3 PRIORITY DATA:
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US/08/904,686
6 FILING DATE: 01-AUG-1990 / 3/24, 977
7 PILING DATE: 18-OCT-1994
8 PILING DATE: 18-OCT-1994
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: JP 2-167466
11 FILING DATE: 31-AUG-1990
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: JP 2-230921
14 FILING DATE: 31-AUG-1990
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: JP 2-305605
17 FILING DATE: 03-NOV-1990
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/099,706
20 FILING DATE: 01-AUG-1990
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/769,996
23 FILING DATE: 02-OCT-1991
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/635,451
26 FILING DATE: 28-DEC-1990
27 ATTORNEY/AGENT INFORMATION:
28 NAME/KEY: 31541
29 REGISTRATION NUMBER: 31541
30 TELECOMMUNICATION INFORMATION:
31 REFERENCE/DOCKET NUMBER: 900703G
32 INFORMATION FOR SEQ ID NO: 1:
33 LENGTH: 1530
34 TYPE: Text
35 TOPOLOGY: linear
36 STRANDEDNESS: single
37 MOLECULE TYPE: cDNA from genomic RNA
38 NAME/KEY: misc feature
39 LOCATION: 1..2991
40 OTHER INFORMATION:
41 COMMENT: (SEQUENCE NOTE)
42 FEATURE:
43 NAME/KEY: CDS

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Qy 1388 TACCTCAGATCATTTGAGACGACTCATGCTGTAGCGATCTTTCACTGCATAGTACTCTCC 1447  
 Db 2594 TACTTCAGATCATTTGAGACGACTCATGCTGTAGCGATCTTTCACTGCATAGTACTCTCC 2653  
 Qy 1448 CAGCTGAGATCATTTGAGACGACTCATGCTGTAGCGATCTTTCACTGCATAGTACTCTCC 1507  
 Db 2654 CAGCTGAGATCATTTGAGACGACTCATGCTGTAGCGATCTTTCACTGCATAGTACTCTCC 2713  
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 Db 2714 TCTGAGACATCATTTGAGACGACTCATGCTGTAGCGATCTTTCACTGCATAGTACTCTCC 2773  
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 Qy 1688 AAT 1721  
 Db 2894 AAT 2927

# RESULT 7

Sequence 35, Application US/08324977

Patent No. 5747339

GENERAL INFORMATION:

APPLICANT: OKAWA, Hiroto

INVENTOR: OKAWA, Hiroto

APPLICANT: OKAWA, Hiroto

APPLICANT: OKAWA, Hiroto

APPLICANT: OKAWA, Hiroto

APPLICANT: OKAWA, Hiroto

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APPLICANT: OKAWA, Hiroto

APPLICANT: OKAWA, Hiroto

APPLICANT: OKAWA, Hiroto

NAME: Stevens-Smith, Theresa M.  
 REFERENCE/DOCKET NUMBER: 900703D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 659-2930  
 TELEFAX: (202) 887-0357  
 TELEX: 44014  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7863 base pairs  
 TYPE: DNA  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA from genomic RNA  
 NAME/KEY: CDS  
 LOCATION: 1..7863  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 7863  
 OTHER INFORMATION: "sequence = 1500 - 9362 of  
 OTHER INFORMATION: SEQ ID NO: 1"  
 US-08-324-977-35

## Query Watch

Best Local Similarity 91.8%

Mismatches 1605; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Qy 68 GCAAGCTGCTCATGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 127

Db 5146 GCAAGCTGCTCATGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 6205

Qy 128 CCACACATCCGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 187

Db 6206 CCACACATCCGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 6265

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Qy 248 AGGCTAACTGCTTCATCATGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 307

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Qy 308 CAAATTTGCTTCATCATGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 367

Db 6386 CAAATTTGCTTCATCATGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 6445

Qy 368 TCTGCTGCTGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 427

Db 6446 TCTGCTGCTGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 6505

Qy 428 TGGCAAAAATGAGGTTTCTGCTGCTGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 487

Db 6506 TGGCAAAAATGAGGTTTCTGCTGCTGAGAGAGGCGCTTCATCATCACTGCTGCTGGAGAAA 6565

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 6866 GGGTCTATATCGGGGTCGATGATCAATCTCAAGGGGAGACTCGGTATCGCGGT 6925  
 948 CCGCGGAGCGGGGTCGATGATCAATCTCAAGGGGAGACTCGGTATCGCGGT 907  
 6926 CCGCGGAGCGGGGTCGATGATCAATCTCAAGGGGAGACTCGGTATCGCGGT 6985  
 908 CCGCGGAGCGGGGTCGATGATCAATCTCAAGGGGAGACTCGGTATCGCGGT 967  
 6986 CCGCGGAGCGGGGTCGATGATCAATCTCAAGGGGAGACTCGGTATCGCGGT 7045  
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 7046 ACTGTGTGTGTATCTGTGAAGTCGGGGGACCCAGAGAGCGCGGACCTACAGATCT 7105  
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 1688 ACATATATCAAGCGCTGTCTGTCGCCCCGACCCCG 1721  
 7766 ACATATATCAAGCGCTGTCTGTCGCCCCGACCCCG 7799

. RESULT 8

US-08-384-616-35  
 Sequence 35, Application US/08384616  
 GENERAL INFORMATION:  
 APPLICANT: OKAYAMA, Hiroto  
 APPLICANT: FURE, Isao  
 APPLICANT: MIKI, Chieko  
 APPLICANT: TAMURA, Akahisa  
 APPLICANT: YOSHIDA, Taro  
 TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
 TITLE OF INVENTION: CDNA AND NON-B HEPATITIS POLYPEPTIDE  
 NUMBER OF SEQUENCE: 10  
 NUMBER OF SEQUENCE: 10  
 ADDRESS: Arnetstrong, Westerman, Hattori, Mcleland &  
 ADDRESS: Naughton  
 STREET: 1725 K St. N.W. Suite 1000  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0  
 OPERATING SYSTEM: IBM PC Compatible  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/384,616  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA: US 07/769,996  
 APPLICATION NUMBER: 02-OCT-1991  
 APPLICATION NUMBER: JP 2-167466  
 FILING DATE: 25-JUN-1990  
 PRIOR APPLICATION DATA: JP 2-230921  
 APPLICATION NUMBER: 31-NOV-1990  
 FILING DATE: 31-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-305605  
 FILING DATE: 09-NOV-1990  
 APPLICATION NUMBER: US 07/635,451  
 FILING DATE: 28-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stearns, W. H.  
 ADDRESS: 1678  
 REFERENCE/DOCKET NUMBER: 900703B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 659-2930  
 TELEFAX: (202) 887-0357  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7663 base pairs  
 TYPE: misc. other  
 STRAIN/GENESIS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA from genomic RNA  
 FEATURES:  
 NAME/KEY: CDS  
 LOCATION: 1..7663  
 NAME/KEY: misc feature  
 LOCATION: 7663  
 OTHER INFORMATION: "sequence = 1500 - 9362 of  
 OTHER INFORMATION: SEQ ID NO: 1"  
 US-08-384-616-35

Query Match 88.5%, Score 1539.6; DB 2; Length 7863;  
 Similarity 93.6%; Pred. No. 0;  
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QY

. RESULT 8









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 7766 ACTATATGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 7799

Patent No. 5747339  
 GENERAL INFORMATION:  
 INVENTOR: KAWAKURA, Hiroko  
 APPLICANT: FUJIE, Isao  
 APPLICANT: MORI, Chiaki  
 APPLICANT: TAKAMIZAWA, Akahisa  
 APPLICANT: YOSHIDA, Masao  
 TITLE OF INVENTION: KONA, NON-B HEPATITIS VIRUS GENOMIC  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Hattori, Westman, Hattori, McJelund &  
 STREET: 1725 K St. N.W. Suite 1000  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 in, 1.44MB  
 COMPUTER: IBM PC compatible  
 SOFTWARE: PC-DOS/MS-DOS, Version 5.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/324,977  
 FILING DATE: 18-JUL-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-167466  
 FILING DATE: 25-JUN-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-230921  
 FILING DATE: 31-AUG-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-305605  
 FILING DATE: 09-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/099,706  
 FILING DATE: 30-JUL-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/769,996  
 FILING DATE: 28-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 36,281  
 REFERENCE/DOCKET NUMBER: 900703D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 887-0350  
 TELEFAX: (202) 887-0357  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 NAME: H12345678910  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA from genomic RNA  
 FEATURE:  
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 NAME/KEY: nice feature  
 LOCATION: 1..7862  
 OTHER INFORMATION: /note="sequence = 1500 - 9416 of  
 OTHER INFORMATION: SEQ ID NO: 1"  
 US-08-324-977-31

Query Match 88.5%; Score 1539.6; DB 1; Length 7917;  
 Best Local Similarity 93.6%; Pred. No. 0;  
 Matches 1605; Conservative 0; Mismatches 109; Indels 0; Gaps 0

[illegible]

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Db	7202	AAAGGCTGTGTACTCTCATCCGCTGATCCACAGCGTCCCTCTTGGCGGGGTGGTGGAGG	72885
Qy	1206	CGCTGCGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG	12677
Db	7286	GACCTAGACAGATCGATTTACTCTTGTCTAGGCAACATCATATGTAATGCGCCACTT	73495
Qy	1268	TGTGGGCAAGGATATCTCTGATATCTACTCTCTCATCTCTCTAGCCAGAGAGCAAT	13271
Db	7346	TGTGGGCAAGGATATCTCTGATATCTACTCTCTCATCTCTCTAGCCAGAGAGCAAT	74055
Qy	1328	TTCGAAAAGCCCTGGATCTCGAATCTAGCGGGCTGTGTACTCCATTAAGGACCATTAACC	13871
Db	7408	TTCGAAAAGCCCTGGATCTCGAATCTAGCGGGCTGTGTACTCCATTAAGGACCATTAACC	74655
Qy	1408	TACTCAGATATGATGACCATCATAGGCTGTAGGGCTGTGTACATTAAGTACTATCTC	14477
Db	7466	TACTCAGATATGATGACCATCATAGGCTGTAGGGCTGTGTACATTAAGTACTATCTC	75255
Qy	1448	CAGTGTGACATAGGCTGGTCAATGCTGACAGAGATGCTGGGATACGCTGCTGGAG	15077
Db	7526	CAGTGTGACATAGGCTGGTCAATGCTGACAGAGATGCTGGGATACGCTGCTGGAG	75895
Qy	1508	TCTGAGACATCGGCTCAGAGATGTCTGCGCTCTAAGTATCTCTGAGCGGGGAGGGCCG	15677
Db	7586	TCTGAGACATCGGCTCAGAGATGTCTGCGCTCTAAGTATCTCTGAGCGGGGAGGGCCG	76455
Qy	1568	CCCTTTGTGGCAGTACTCTCAATCTGGGACGTGAAGGACCAAGCTTAAATCTATCGAA	16277
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Qy	1628	TTCGGGCTCGCTCGGGCTGCACTTATGCGGCTGGTCTGCTGCTCAGAGCGGGGAG	16887
Db	7708	TTCGGGCTCGCTCGGGCTGCACTTATGCGGCTGGTCTGCTGCTCAGAGCGGGGAG	77655
Qy	1688	ACATATATACAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1721
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RESULT 12  
US-08-384-616-31  
Sequence 31, Application US/08394616  
1. GENERAL INFORMATION:  
APPLICANT: OKAWAMA, Hiroko  
APPLICANT: FUKU, Ideo  
APPLICANT: KAWABATA, Akieko  
APPLICANT: TAKAMIZAWA, Akahisa  
APPLICANT: YOSHIDA, Iwao  
2. TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
SEQUENCE, AND ANTIGEN POLYPEPTIDE  
3. NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Armstrong, Westerman, Hattori, McLeod and  
STREIBER 1725 W. St. N.W. Suite 1000  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: ASCII, PC-DOS/MS-DOS, Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/384-616









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 ? PRIOR APPLICATION DATA: JP 2-230921  
 ? PILING DATE: 31-AUG-1990  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: JP 2-305605  
 ? PILING DATE: 25-JUN-1990  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 08/099,706  
 ? PILING DATE: 30-JUL-1993  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/769,996  
 ? PILING DATE: 02-OCT-1991  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/635,451  
 ? PILING DATE: 28-DEC-1990  
 ? APPLICATION DATA:  
 ? NAME: Scavone-Smith, Theresa M.  
 ? REFERENCE/DOCKET NUMBER: 36,281  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (202) 897-0157  
 ? TELEFAX: (202) 897-0157  
 ? TELEX: 440142  
 ? INFORMATION FOR SEQ ID NO: 13:  
 ? SEQUENCE CHARACTERISTICS:  
 ? TYPE: linear  
 ? STRANDEDNESS: single  
 ? TOPOLOGY: linear  
 ? MODIFICATION TYPE: cDNA from genomic RNA  
 ? FEATURES:  
 ? NAME/KEY: misc feature  
 ? LOCATION: 1..5030  
 ? OTHER INFORMATION: /note="sequence = 333 - 9362 of  
 ? SEQUENCE INFORMATION: SEQ ID NO: 1"  
 ? NAME/KEY: CDS  
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 ? US-08-324-977-13

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 ACCESSION AF165063  
 VERSION 1  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REFERENCE Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepicivirus (to 9379)  
 AUTHORS Nagayama K., Kurotsaki M., Enomoto N., Maekawa S.Y., Miyasaka Y., Tazawa J., Izumi N., Marumo F. and Sato C.  
 TITLE Time-related changes in full-length hepatitis C virus sequences and hepatitis activity  
 JOURNAL JOURNAL  
 MEDLINE 2001325  
 PUBMED 1054098  
 REFERENCE 2 (bases 1 to 9379)  
 AUTHORS Nagayama K., Kurotsaki M., Enomoto N., Maekawa S., Miyasaka Y., Tazawa J., Izumi N., Marumo F., and Sato C.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1999) Second Department of Internal Medicine, Tokyo Medical and Dental University, 1-5-45 Yushima Bunkyo-ku, Tokyo 113-8519, Japan  
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 1. 9379 Qualifiers  
 /organism="Hepatitis C virus"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:11103"  
 /note="from a patient with persistently high serum ALT values; patient 8, point 2 genotype: 1b"

[illegible]











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ORIGIN  
 Query Match 89.7%; Score 1617.8; DB 14; Length 9375;  
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 Matches 1676; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
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[illegible]

REFERENCE	1 (bases 1 to 9448)	Hepacivirus.
AUTHORS	Okamoto,H., Kojima,M., Okada,S., Yoshizawa,H., Iizuka,H., Tanaka,H., Taniuchi,K., Peterson,D.R., Ito,K. and Minato,S.	
TITLE	Genomic organization and sequencing of a 9.5-year infection in a chimpanzee: variability and stability	
JOURNAL	Virology 190 (2), 894-899 (1992)	
MEDLINE	9239112	
PMID	1327113	
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Scoring table: IDENTITY NUC  
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Searched: 34239544 seqs, 19032134700 residues 68475088

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1: gb.est.1.\*  
2: gb.est.2.\*  
3: gb.hic.\*  
4: gb.hic.1.\*  
5: gb.est.1.\*  
6: gb.est.2.\*  
7: gb.est.1.\*  
8: gb.gesi.\*  
9: gb.gesi.\*

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# SUMMARIES

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4	40.6	2.3	593	CA390175	AGENCOURT
5	40.6	2.3	593	CA390175	ch107d09.
6	39.9	2.2	487	EX262027	AGENCOURT
7	39.9	2.2	685	EX262027	AGENCOURT
8	39.9	2.2	820	CA391891	AGENCOURT
9	39.9	2.2	820	CA391891	AGENCOURT
10	39.9	2.2	820	CA391891	AGENCOURT
11	39.9	2.2	918	BQ720502	AGENCOURT
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13	39.9	2.2	954	BQ738788	AGENCOURT
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18	39.9	2.2	1740	CA391576	full-length
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21	39.9	2.2	1753	CA392474	full-length
22	39.9	2.2	1753	CA390948	full-length
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27	38.4	2.1	1071	8	AF094875	pp2n-pko
28	38.4	2.1	288	2	BB38875	AF094871
29	38.4	2.1	1071	8	AF094871	AF094871
30	38	2.1	403	8	AQ936657	AQ936657
31	38	2.1	509	1	A1657258	486092F08
32	38	2.1	509	1	A1657258	486092F08
33	37.8	2.1	612	2	BE987710	BE987710
34	37.8	2.1	772	9	CNS02XEP	AL218266
35	37.8	2.1	869	9	CNS03M08	AL263969
36	37.8	2.1	1072	5	CNS03M08	AL166305
37	37.8	2.1	1072	5	CNS03M08	AL166305
38	37.4	2.1	259	8	A2665259	AL218266
39	37.4	2.1	546	2	A2655326	AL263969
40	37.4	2.1	905	9	AQ042203	AL263969
41	37.4	2.1	958	4	BT286622	AL169502
42	37.2	2.1	958	4	BT286622	AL169502
43	37.2	2.1	1007	5	BQ672629	BQ672629
44	37.2	2.1	1100	9	CA3901491	AL104520
45	37	2.1	274	9	CE434162	Drosophill

## ALIGNMENTS

AL516365 Homo sapiens NEUROBLASTOMA 891 bp mRNA linear EST 21-MAR-2004  
CS00A005J06 5-PRIME, mRNA sequence.  
AL516365.3 GI:45653002  
EST.  
Homo sapiens (human)  
Homo sapiens  
Mus musculus  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Rodentia; Muridae; Murinae; Cricetidae; Cricetini; Hominidae; Homo.  
1 (bases 1 to 891)  
L.I.W.B., Gamber, C.J., Jessee, J., and Polayes, D.  
Unpublished (2001) libraries and normalization  
On Feb 13, 2001 this sequence version replaced gi:30490324.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
Genoscope, 25 Avenue de l'Europe, 91061 Evry-Courcouronnes, France  
E-mail: seqgen@genoscope.fr Web: http://www.genoscope.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
size of Invitrogen library was constructed by Life Technologies, a  
division of Invitrogen to sequence cluster 6432.r  
This sequence belongs to sequence cluster 6432.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdnas/CS00A005J06Q1021c=6432.r.

## FEATURES

1..891  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/db\_xref="GeneID:45653002"  
/tissue="NEUROBLASTOMA"  
/clone\_lib="Homo sapiens NEUROBLASTOMA"  
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and EcoRV sites  
of the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

## ORIGIN

Query Match 2.5%; Score 45.4; DB 1; Length 891;  
Best Local Similarity 47.8%; Pred. No. 0.19;  
Matches 118; Conservative 3; Mismatches 126; Indels 0; Gaps 0;



FEATURES	Location/Qualifiers
source	1. .665











## ORIGIN

Query Match 2.2%; Score 39; DB 5; Length 954;  
 Best Local Similarity 47.4%; Pred. No. 15;  
 Matches 117; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

Qy 37 GCCTGATGACACCTGCGTGGGAGGAGGAGGCTCCCAACAGCGCTGAGCAAC 96  
 Db 272 GCGCGCTCTGACCGATCTGGGAGGAGGAGGAGGCTCCCAACAGCGCTGAGCAAC 331

Qy 97 TCTTCTGCTGGTCAACAACTGCTGTATCAACAATCCCGAGTGAAGCTCGG 156  
 Db 332 TCTGCTCTCTCCGAGAGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 391

Qy 157 CAGAGAGAGTCACTTTTGAAGAGTCAAGCTCTGAGAGCATTAACCGAGCTCTC 216  
 Db 392 AAGATGAGTCTTCTGATGATGAGATTAAGTCTTCAAGAGCTGCGAGAGAGCTG 451

Qy 217 AAGAGATGAGAGGAGGCTCCACAGTGAAGCTAACTGCTATGAGAGAGCA 276  
 Db 452 CGAGAGCTGCAAGTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 511

Qy 277 TGTGAGC 283  
 Db 512 GTGAGC 518

## RESULT 14

BE263117 993 bp mRNA linear SST 13-JUL-2000  
 LOCUS full-length cDNA clone C6014428F2 NIH\_MGC\_19 Homo sapiens cDNA IMAGE:3160350 5',  
 3' UTR, complete cds.  
 DEFINITION M584 sequence.  
 ACCESSION BE263117.1 GI:9136653  
 VERSION BE263117.1 GI:9136653  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

1. (bases 1 to 993)  
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/  
 Bases 1 to 993  
 Unpublished (1999)  
 Contract: Robert Strausberg, Ph.D.  
 Email: csp@b6-remail.nih.gov  
 Plate: LIC6116 row: 9 col: 699  
 High quality  
 Location/Qualifiers

## FEATURES

source 1..993  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cldna="IMAGE:3160350"  
 /lab\_host="PHIB (phage-resistant)"  
 /note="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adapter: GCGACGCG (G) library constructed by Hong Hong (California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 2.2%; Score 39; DB 2; Length 993;  
 Best Local Similarity 47.4%; Pred. No. 15;  
 Matches 117; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

Qy 37 GCCTGATGACACCTGCGTGGGAGGAGGAGGCTCCCAACAGCGCTGAGCAAC 96  
 Db 339 GCGCGCTCTGACCGATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398

Qy 97 TCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 156  
 Db 399 CTCCTCTCTCCGAGAGGATGAGCAATGCTCAATCTCTCTCTCTCTCTCTCTCT 216

Qy 157 CAGAGAGAGTCACTTTTGAAGAGTCAAGCTCTGAGAGCATTAACCGAGCTCTC 276  
 Db 458 AAGATGAGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 519

Qy 217 AAGAGATGAGAGGAGGCTCCACAGTGAAGCTAACTGCTATGAGAGAGCA 276  
 Db 519 CGAGAGCTGCAAGTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 576

Qy 277 TGTGAGC 283  
 Db 579 GTGAGC 585

## RESULT 15

CR620795 1606 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone C6014010V118 of Neuroblastoma of Homo sapiens (human).  
 DEFINITION CR620795  
 ACCESSION CR620795.1 GI:50501602  
 VERSION CR620795.1 GI:50501602  
 KEYWORDS HTC; Neuroblastoma; Homo sapiens  
 ORGANISM Homo sapiens

## REFERENCE

1. (bases 1 to 1606)  
 Genoscope  
 Genoscope  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage  
 BP 91 91006 EVRY cedex - FRANCE (E-mail : se@ref.genoscope.cns.fr)  
 Web : www.genoscope.cns.fr)  
 The strand cDNA was primed with a NotI-oligo(dT) primer. Five primers into the NotI and EcoRV sites of the pCNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen

## FEATURES

source Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cldna="Genoscope"  
 /cldna\_type="Neuroblastoma"  
 /plasmid="pCNSPORT\_6"

## ORIGIN

Query Match 2.2%; Score 39; DB 3; Length 1606;  
 Best Local Similarity 47.4%; Pred. No. 18;  
 Matches 117; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

Qy 37 GCCTGATGACACCTGCGTGGGAGGAGGAGGCTCCCAACAGCGCTGAGCAAC 478  
 Db 419 GCGCGCTCTGACCGATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 478

Qy 97 TCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 156  
 Db 479 CTCCTCTCTCCGAGAGGATGAGCAATGCTCAATCTCTCTCTCTCTCTCTCTCT 538

Qy 157 CAGAGAGAGTCACTTTTGAAGAGTCAAGCTCTGAGAGCATTAACCGAGCTCTC 216  
 Db 539 AAGATGAGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 598

DY 217 AAGGAGATGAGCGGAGGCTCCACAGTGAAGCTTAAGCTGCTATCTGTGAGAGCA 276  
DB |||||  
QY 599 CGAGAGCTCGAGTGTGAGAGCCAGAGTGCAGAGTGGAGGTGAGCCACG 658  
DB |||||  
QY 277 TGCAGGC 283  
DB |||||  
DB 659 GTGAAGC 665

Search completed, October 3, 2005, 22:17:00  
Job time : 6154.94 secs

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Db 1741 CTCCTACTCTCTGAGGAGTGGAGCTGCTATCTATCTCCCAACGGGATCACTACCAT 1800  
 Qy 1801 CAC 1803  
 Db 1801 CAC 1803

RESULT 2  
 ADO19022  
 XX ADO19022 standard; DNA; 1740 BP.  
 AC ADO19022;  
 XX  
 XT 12-AUG-2004 (first entry)  
 DE DNA encoding C-terminally truncated HCV NS5B polymerase, Cdelta21 NSB.  
 XX  
 KW RNA polymerase activity; continuous-read assay;  
 KW Hepatitis C virus infection; HCV infection; polymerase; NS5B;  
 KW diabetes; ocular disorder; renal dysfunction; cardiovascular disease;  
 KW lymphoproliferative disorder; metabolic disorder; arthritis;  
 KW sleep disorder; thyroid disorder; antiinflammatory; hepatotropic;  
 KW virulence; osteopathic; cytotoxic; antidiabetic; ophthalmological;  
 KW nephrotropic; antiarthritis; gene; db.  
 XX  
 OS Hepatitis C virus.

XX Key Location/Qualifiers  
 XX CDS /start=140  
 XX F1 /tag=a  
 XX F2 /partial  
 XX F3 /product="Cdelta21 NSB"  
 XX F4 /note="This sequence lacks a stop codon"  
 XX  
 XX WO2004/041228-A2.  
 XX  
 XX 27-MAY-2004.  
 XX  
 XX 13-NOV-2003; 2003NO-US0316465.  
 XX  
 XX 13-NOV-2002; 2002US-0425981P.  
 XX  
 XX (PFI2) PFIZER INC.  
 XX  
 XX Yagi Y, Sheets MP, Wells PA, Shelly JA, Poorman RA, Epps DE,  
 XX Morgan AG;  
 XX WPI; 2004-420317/39.  
 XX P-FSDB; ADO19023.  
 XX  
 XX Detecting RNA polymerase activity in a continuous-read manner, useful in  
 XX treating osteoporosis, carcinomas, cardiovascular diseases, ocular  
 XX disorders, and other diseases by contacting an RNA polymerase with an  
 XX oligonucleotide template.  
 XX  
 XX Disclosure; SEQ ID NO 3; 46pp; English.

CC The present invention relates to a method for detecting RNA polymerase  
 CC activity in a continuous-read manner. The method comprises: (a) using an  
 CC RNA polymerase with an oligonucleotide template in a reaction mixture  
 CC comprising an assay buffer, under conditions in which the RNA polymerase  
 CC catalyzes the synthesis of a double-stranded nucleic acid molecule, the  
 CC nucleic acid molecule being capable of binding double-stranded  
 CC fluorescence of the reaction mixture. The RNA polymerase is the Hepatitis  
 CC C virus (HCV) polymerase, NS5B. The method is useful for treating HCV  
 CC infection, bone mineral diseases like osteoporosis, carcinomas,  
 CC infectious diseases like osteomyelitis, ocular disorders, renal dysfunction,  
 CC lymphomas, lymphoproliferative disorders, and other diseases, and  
 CC sleep disorders and thyroid disorders. The present sequence encodes C-  
 CC terminally truncated HCV NS5B polymerase (designated Cdelta21 NSB).  
 CC  
 XX Sequence 1740 BP; 404 A; 509 C; 457 G; 370 T; 0 U; 0 Other;

Query Match  
 95.5%; Score 1722; DB 12; Length 1740;  
 Similarity 100.0%; Pred. No. 0;  
 Matches 1722; Conservative 0; Ploppatches 0; Gaps 0;

Oy 1 ATGGCTAGCATGTCATATGCTCTATATGAGAGAGGGCCCTGATCAGCGTGGCTGGG 60  
 Db 1 ATGGCTAGCATGTCATATGCTCTATATGAGAGAGGGCCCTGATCAGCGTGGCTGGG 60  
 Qy 61 GAGGAAAGCAAGCTGCCATCAAGGGCTGAGACATCTCTGCTGTCACATCACTG 120  
 Db 61 GAGGAAAGCAAGCTGCCATCAAGGGCTGAGACATCTCTGCTGTCACATCACTG 120  
 Qy 121 GTCTATTCACACATCCCGGCTGCAAGCTCCGGGCAAGAGAGTCACTTTGACGGA 180  
 Db 121 GTCTATTCACACATCCCGGCTGCAAGCTCCGGGCAAGAGAGTCACTTTGACGGA 180  
 Qy 181 CTCGAAGTCTGAGCATATTAACCGGAGCTGCTGAGAGAGTGAAGGCGGCTCC 240  
 Db 181 CTCGAAGTCTGAGCATATTAACCGGAGCTGCTGAGAGAGTGAAGGCGGCTCC 240  
 Qy 241 AAGTGAAGCTGTAATCTGCTATCTGTGAGAGAGAGCTGATGAGCTGCTGCTG 300  
 Db 241 AAGTGAAGCTGTAATCTGCTATCTGTGAGAGAGAGCTGATGAGCTGCTGCTG 300  
 Qy 301 GCGAATCAATTTGGCTGCTGAGAGAGAGCTGCTGAGAGAGCTTCAAGAGGGCGTT 360  
 Db 301 GCGAATCAATTTGGCTGCTGAGAGAGAGCTGCTGAGAGAGCTTCAAGAGGGCGTT 360  
 Qy 361 AAGCAATCTCTGCTGCTGAGAGAGCTGCTGAGAGAGCTGACACACCACTACAGAC 420  
 Db 361 AAGCAATCTCTGCTGCTGAGAGAGCTGCTGAGAGAGCTGACACCACTACAGAC 420  
 Qy 421 ACCATCACTGGGAAAATGAGGTTTCTGCTCAACAGAGAGAGAGGGCGGAAACCA 480  
 Db 421 ACCATCACTGGGAAAATGAGGTTTCTGCTCAACAGAGAGAGAGGGCGGAAACCA 480  
 Qy 481 GCTGCTCATCATGATATCCAGAGAGCTGGAGAGTCTGCTGTAAGAGAGAGTGCCTTAC 540  
 Db 481 GCTGCTCATCATGATATCCAGAGAGCTGGAGAGTCTGCTGTAAGAGAGAGTGCCTTAC 540  
 Qy 541 GAGGTGGTTTCACTCTCTCAAGGCGTGTAGTGGCTCTCACTACGATTCGATATCT 600  
 Db 541 GAGGTGGTTTCACTCTCTCAAGGCGTGTAGTGGCTCTCACTACGATTCGATATCT 600  
 Qy 601 CTTAAGAGAGCGGTGAGGTTCTGCTGATATCTGGAAGCAAGCAAGAAATCTCTATGGC 660  
 Db 601 CTTAAGAGAGCGGTGAGGTTCTGCTGATATCTGGAAGCAAGCAAGAAATCTCTATGGC 660  
 Qy 661 TTCTAT 720  
 Db 661 TTCTAT 720  
 Qy 721 GACTCAATTTACCAATGTTGATCTGGCTGGCCGAGAGCTAGACAGGCGCAATAGTGCCTC 780  
 Db 721 GACTCAATTTACCAATGTTGATCTGGCTGGCCGAGAGCTAGACAGGCGCAATAGTGCCTC 780  
 Qy 781 AAGAGAGGGCTCTATATCTGGGGGCTCCATATCACTCAAGAGAGGCAAGATCGGGCTAT 840  
 Db 781 AAGAGAGGGCTCTATATCTGGGGGCTCCATATCACTCAAGAGAGGCAAGATCGGGCTAT 840  
 Qy 841 GCGGCTGCGGGGAGAGCGGCTGCTGAGAGCTAGCTGGTATATACCTCACTAGCTGAC 900  
 Db 841 GCGGCTGCGGGGAGAGCGGCTGCTGAGAGCTAGCTGGTATATACCTCACTAGCTGAC 900  
 Qy 901 TTGAAGAGCGGCTGAGCTGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 960  
 Db 901 TTGAAGAGCGGCTGAGCTGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 960  
 Qy 961 GAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 Db 961 GAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020





464	TCGGCTCCGCTGGAGGACTGCTGGAGACATGAGACACCAATGACACACCACTCA	523	1508	TCCTGAGACATGGGCGGAGAGTGTCCGCTGCTAGTCTGCTGGAGGCGGAGGCGG	1567
465	TGCGAAAAATATGCTTTCTTCGTTCCATCCAGACGAGAGGCGGCGAAACAGCTGCC	487	1604	TCCTGAGACATGGGCGGAGAGTGTCCGCTGCTAGTCTGCTGGAGGCGGAGGCGG	1663
524	TGCGAAAAATATGCTTTCTTCGTTCCATCCAGACGAGAGGCGGCGAAACAGCTGCC	583	1568	CGATTTCTGCGACGATCTCTTCACTGCGGCGGAGAGGAGGAGGATTAAGTCTCTGGA	1627
488	TGATGATATCTCCAGACGATGGAGATCTGTTGATGCGAGAGATGGCCTTTAGAGATGG	547	1664	CTTCTGCGGATGAGTCTCTTCACTGCGGCGGAGAGGAGGAGGATTAAGTCTCTGGA	1723
584	TGATGATATCTCCAGACGATGGAGATCTGTTGATGCGAGAGATGGCCTTTAGAGATGG	643	1628	TCCTGAGACATGGGCGGAGAGTGTCCGCTGCTAGTCTGCTGGAGGCGGAGGCGG	1783
548	TTTCGACATCTCTCCAGGCGGATGAGGGCTCTCATAGGATTCGATCTCTCCAGC	607	1724	TCCTGAGACATGGGCGGAGAGTGTCCGCTGCTAGTCTGCTGGAGGCGGAGGCGG	1783
608	TCCTGACATCTCTCCAGGCGGATGAGGGCTCTCATAGGATTCGATCTCTCCAGC	703	1688	AGATATATGACGCTCTCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1747
644	AGCGGTCGACCTCTGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	667	1784	AGATATATGACGCTCTCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1843
704	AGCGGTCGACCTCTGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	763	1748	TCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1784
668	ATGACGACCGCGGTTTGTGACATCAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGG	727	1844	TTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1880
764	ATGACGACCGCGGTTTGTGACATCAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGG	823			
728	TTTACGATGCTGTGACATCAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	783			
824	TCTACCAATGTTGTACTTGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	883			
788	GGCTATATGCTGGGATCTCCATGATCTACTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGG	847			
884	GGCTATATGCTGGGATCTCCATGATCTACTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGG	943			
848	CGCGCGCGCGGGGCTGACGATGAGCTGCGGTATATCCCTCATCTACTTCTAGAGG	907			
944	CGCGCGCGCGGGGCTGACGATGAGCTGCGGTATATCCCTCATCTACTTCTAGAGG	1003			
908	CGCGCGCGCGGGGCTGACGATGAGCTGCGGTATATCCCTCATCTACTTCTAGAGG	967			
1004	CTCTGCGGCTGTCGACGCTGCGAGCTGCGAGCTGCGAGCTGCTGTTGAGGAGGAGGAGG	1063			
968	ACCTGCTGCTTATCTGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1027			
1064	ACCTGCTGCTTATCTGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1123			
1028	TCACGAGGAGCTATGATGAGTACTTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1087			
1124	TCACGAGGAGCTATGATGAGTACTTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1183			
1088	ACTTGGAGCTGATGAGTACTTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1147			
1184	ACTTGGAGCTGATGAGTACTTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1243			
1148	ACTTGGAGCTGATGAGTACTTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1207			
1244	AAAGGGGTGATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	1303			
1208	CAGCTAGGAGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	1267			
1304	CAGCTAGGAGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	1363			
1268	TGTCGAGGAGGAGGATGATGAGTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1327			
1364	TGTCGAGGAGGAGGATGATGAGTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1423			
1328	TGTCGAGGAGGAGGATGATGAGTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1387			
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1388	TACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	1447			
1484	TACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT	1543			
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[illegible][illegible]













PN M02003085084-A2.  
 XX 16-OCT-2003.  
 XX 03-APR-2003; 2003MO-U8010137.  
 XX 03-APR-2002; 2002US-0369685P.  
 XX (SMIX) SNTUKLINE BECHAM CORP.  
 PA Gates A, Gu B, Sariisky RT;  
 PI WPI; 2003-804301/75.  
 DR  
 XX  
 PT New hepatitis C virus (HCV) sub-genomic replicon, useful for facilitating  
 screening or testing of anti-HCV drugs, comprises a nucleic acid  
 sequence encoding chimeric HCV non-structural proteins, and an NS5B  
 polymerase gene.  
 PT  
 XX  
 XX Disclosure; Page 70-75; 159pp; English.  
 XX The present sequence comprises a replicating hepatitis C virus (HCV) 3'  
 CC replicon. The invention provides sub-genomic replicons of HCV containing  
 CC a nucleic acid construct encoding chimeric HCV nonstructural protein and  
 CC an NS5B polymerase gene. A preferred replicon comprises an N63 nucleotide  
 CC sequence ABB3371 that encodes the first 75 contiguous N-terminal amino  
 CC residues of the NS5B polymerase. The NS5B polymerase replicon may  
 CC comprise an N83 sequence from any of the 6 major HCV genotypes and  
 CC subtypes but has its first 125 nucleotides of the coding sequence  
 CC replaced by the 887 strain NS5B sequence, especially where the replicon is  
 CC from HCV genotype 1a (H77 strain) or genotype 1b (O4 strain). Stable cell  
 CC lines expressing the replicon are provided. The NS5B polymerase replicon  
 CC sequences from HCV genotype 1a (strain H77) or genotype 1b (strain J4)  
 CC within the prototype 1b replicon backbone from HCV strain H87 are  
 CC provided. These can be used to screen for compounds that modulate viral  
 CC replication. The sub-genomic HCV replicon systems of the invention may  
 CC be used to study the function of the NS5B polymerase and the NS5A  
 CC genotypes and subtypes to facilitate screening, testing and evaluating  
 CC anti-infective agents for HCV disease (e).  
 XX  
 XX Sequence 7979 BP; 1674 A; 2351 C; 2216 G; 1738 T; 0 U; 0 Other;  
 SQ  
 Query Match 88.5%; Score 1596.2; DB 10; Length 7979;  
 Best Local Similarity 93.6%; Pred. No. 0;  
 Matches 1664; Conservative 0; Mismatches 113; Indels 0; Gaps 0;  
 OY 8 GCGATGTCATGCTCTATACATGACAGCGCCCTGATCACACCTGGCGCGAGAA 67  
 5978 GCGTCGTCGTCATGTCATGACAGCGCCCTGATCACACCTGGCGCGAGAA 6037  
 OY 66 GCGAGCGTCGTCATGTCATGACAGCGCCCTGATCACACCTGGCGCGAGAA 127  
 6038 GTAGCGTCGTCATGTCATGACAGCGCCCTGATCACACCTGGCGCGAGAA 6097  
 OY 128 GCGAGTCGTCGTCATGTCATGACAGCGCCCTGATCACACCTGGCGCGAGAA 187  
 6098 GCGAGTCGTCGTCATGTCATGACAGCGCCCTGATCACACCTGGCGCGAGAA 6157  
 OY 188 TCGTCGAGCATATACCGGAGCGTCTCAAGGAGATGAAGGCGAGGCTCCACGTA 247  
 6158 TCGTCGAGCATATACCGGAGCGTCTCAAGGAGATGAAGGCGAGGCTCCACGTA 2617  
 OY 248 AGCTCAATCTGCTATCTGAGAGAGCGCTGCGAGCGCTCCGCGAGGCTCCACGTA 307  
 6218 AGCTCAATCTGCTATCTGAGAGAGCGCTGCGAGCGCTCCGCGAGGCTCCACGTA 3277  
 OY 308 CCAATTTGGCTATGGGCGAGAGAGCTCCGAGCGCTCCGCGAGGCTCCACGTA 367  
 6278 CCAATTTGGCTATGGGCGAGAGAGCTCCGAGCGCTCCGAGCGCTCCACGTA 437  
 OY 376 TCCGCTGCTGGAGAGAGCTCTGGAGAGAGCTCCGAGCGCTCCGAGCGCTCCACGTA 437  
 6338 TCCGCTGCTGGAGAGAGCTCTGGAGAGAGCTCCGAGCGCTCCGAGCGCTCCACGTA 4597  
 DB

OY 428 TGGCAAAATGAGGTTTCTGGCTCGACCGAGAAAGGCGGCAACGAGCTGGCC 487  
 6398 TGGCAAAATGAGGTTTCTGGCTCGACCGAGAAAGGCGGCAACGAGCTGGCC 6457  
 OY 488 TCGTGTATTCCGACAGCTGGAGTTTCTGTATTCGAGAGATGGCCCTTTACGAGTGG 547  
 6458 TTTTGTATTCCGACAGCTGGAGTTTCTGTATTCGAGAGATGGCCCTTTACGAGTGG 6517  
 OY 548 TTTTCACTCTCTTCGAGCGCTGAGTGGGCTCTCTACAGGATCCAAATCTCTCAAGC 6017  
 6518 TGTCAACCTCTCTTCGAGCGCTGAGTGGGCTCTCTACAGGATCCAAATCTCTCAAGC 6577  
 OY 608 AGCGGTCGAGTTCTGGTGAATACCTGGAAGCAAGAGAAATGCCCATATGGCTCTCAT 667  
 6578 AGCGGTCGAGTTCTGGTGAATACCTGGAAGCAAGAGAAATGCCCATATGGCTCTCAT 6637  
 OY 668 ATGACGCTGGTGTCTGTGATCTCAAGTTCATGGAATCAAGAGAAATGCCCATATGGCTCTCAT 727  
 6638 ATGACGCTGGTGTCTGTGATCTCAAGTTCATGGAATCAAGAGAAATGCCCATATGGCTCTCAT 6597  
 OY 728 TTTTCACTCTCTTCGAGCGCTGAGTGGGCTCTCTACAGGATCCAAATCTCTCAAGC 787  
 6698 TTTTCACTCTCTTCGAGCGCTGAGTGGGCTCTCTACAGGATCCAAATCTCTCAAGC 6757  
 OY 788 GCTCTATCTTCGAGCGCTCCCATGATCTCTCAAGGCGAGAACTGGGCTATGCGCGT 847  
 6758 GCTCTATCTTCGAGCGCTCCCATGATCTCTCAAGGCGAGAACTGGGCTATGCGCGT 6817  
 OY 848 CGCGCGAGAGCGCTGCTGAGCTAGCTGGTGAATACCTCACATGCTACTTCAAGG 907  
 6818 CGCGCGAGAGCGCTGCTGAGCTAGCTGGTGAATACCTCACATGCTACTTCAAGG 6877  
 OY 908 CGCTCGACGCTCTCGAGCTGCACAGCTCCAGAGACTCGAGATGCTCGTGAATGAGAG 967  
 6878 CGACTGCGCTCTCGAGCTGCACAGCTCCAGAGACTCGAGATGCTCGTGAATGAGAG 6937  
 OY 968 ACCTGTGCTTATCTGTGAAGCGCGGAGAACCCAGAGGAGTGGCGGCTCTAGAGCT 1027  
 6938 ACCTGTGCTTATCTGTGAAGCGCGGAGAACCCAGAGGAGTGGCGGCTCTAGAGCT 6997  
 OY 1028 TCGACGAGCTGTATGATCTGCTGAGCGCTGGGCGCTCGGCGCGCGAGCGAGATG 1087  
 6998 TCGACGAGCTGTATGATCTGCTGAGCGCTGGGCGCTCGGCGCGCGAGCGAGATG 7057  
 OY 1088 ACTGTCGAGCTGTATGATCTGCTGAGCGCTGGGCGCTCGGCGCGCGAGCGAGATG 1147  
 7058 ACTGTCGAGCTGTATGATCTGCTGAGCGCTGGGCGCTCGGCGCGCGAGCGAGATG 7117  
 OY 1148 AAGGCTGTACTTCTTCACTGTCGAGCGCGCGCTCGGCGCGCGAGCGAGATG 1207  
 7118 AAGGCTGTACTTCTTCACTGTCGAGCGCGCGCTCGGCGCGCGAGCGAGATG 7177  
 OY 1208 CAGTAGGCGACATCAAGTCAATCTCGCTGAGGAGCAATCATATATATATGGGCGACT 1267  
 7178 CAGTAGGCGACATCAAGTCAATCTCGCTGAGGAGCAATCATATATATATGGGCGACT 7237  
 OY 1268 TGTGGGCAAGAGATTTGATGATCACTCACTTCTTCATCTCTTACGCGAGAGCAAC 1327  
 7238 TATGGGCAAGAGATTTGATGATCACTCACTTCTTCATCTCTTACGCGAGAGCAAC 7297  
 OY 1328 TTTGAAAGCGCTGGATGTGCAGATCTAGAGGGGCTTGTACTCATATGAGCCTATGAGC 1387  
 7298 TTTGAAAGCGCTGGATGTGCAGATCTAGAGGGGCTTGTACTCATATGAGCCTATGAGC 7357  
 OY 1388 TACTCTGAGTCAATGATCTGATCTGATCTAGGCGCTTCTGCTCATCTGATGAGCCTATGAGC 1447  
 7358 TACTCTGAGTCAATGATCTGATCTGATCTAGGCGCTTCTGCTCATCTGATGAGCCTATGAGC 7417  
 OY 1448 CAGTGTGAGTCAATGATCTGATCTGATCTAGGCGCTTCTGCTCATCTGATGAGCCTATGAGC 1507  
 7418 CAGTGTGAGTCAATGATCTGATCTGATCTAGGCGCTTCTGCTCATCTGATGAGCCTATGAGC 7477

OY 1508 TCTGGACATCCGGCAGAGTGTCCGCTACTTACTTCTCCAGCGGGGAGGGCCG 1567  
 DB 7478 CTTGGAGACATCGGGCGAGAGTGTCCGCTACTTACTTCTCCAGCGGGGAGGGCCG 7537  
 OY 1568 CGATTGTGGCAAGTACTCTTCACTGGGCACTAAGCAAGCTTAATCACTCTCAA 1627  
 DB 7538 CCAATGTGGCGAGTACTCTTCACTGGGCACTAAGCAAGCTTAATCACTCTCAA 1597  
 OY 1628 TCCGCGCGGCTCCCGCGGAGCTTATTCGCGGTGTCTGCTGCTACAGCGGGGAG 1687  
 DB 7598 TCCCGCGCGGCTCCCGCGGAGCTTATTCGCGGTGTCTGCTGCTACAGCGGGGAG 7657  
 OY 1688 ACATATATACAGCGCTGTCTGCGCGGAGCGCGCGGTGTCTGCTGCTACTCTCTAC 1747  
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 OY 1748 TTTCTGTAAGCGGTAGGATATATATATATATATATATATATATATATATATAT 1794  
 DB 7718 TTTCTGTAAGCGGTAGGATATATATATATATATATATATATATATATATATAT 7754

## RESULT 12

AAK214843

ID AAK214843 standard; DNA; 9595 BP.

XX AAK214843;

XX AAK214843;

XX AAK214843;

XX AAK214843;

XX AAK214843;

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XX AAK214843;

XX AAK214843;

XX AAK214843;

XX AAK214843;

CC suitable for vaccine development. Infectious nucleic acid sequences can  
 CC also be used to produce attenuated virus via passage in vitro or in vivo  
 CC in cell culture. Infectious nucleic acid sequences can be used to produce  
 CC infectious nucleic acid sequence. Vaccines comprising one or more  
 CC polypeptides made from the infectious nucleic acid sequence are used to  
 CC immunize mammals, especially humans, against hepatitis C. The nucleic  
 CC acid sequences can also be used to produce procedures for immunizing  
 CC against hepatitis C. The nucleic acid sequences can also be used to  
 CC produce procedures for immunizing against hepatitis C. The nucleic  
 CC acid sequences can additionally be used to develop screening assays to  
 CC identify antiviral agents for HCV  
 XX  
 XX Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 U; 0 Other;  
 Query Match  
 Best Local Similarity 93.6%; Score 1596.2; DB 2; Length 9595;  
 Matches 1664; Conservative 0; Mismatches 113; Indels 0; Gaps 0;  
 OY 8 CGATGTCATGCTTATCATGACGAGCGCCCTGATCAGCAGCTGCTGCGGAGGAA 67  
 DB 7594 GCTGCTCAATGCTTATCATGACGAGCGCCCTGATCAGCAGCTGCTGCGGAGGAA 7653  
 OY 68 CGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127  
 DB 7654 GTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1713  
 OY 128 CACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187  
 DB 7714 CACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7773  
 OY 188 TCTGCGAGCTATATACGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247  
 DB 7774 TCTGCGAGCTATATACGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7833  
 OY 248 AGCTTAACTGCTTATCATGACGAGCGCCCTGATCAGCAGCTGCTGCGGAGGAA 307  
 DB 7834 AGCTTAACTGCTTATCATGACGAGCGCCCTGATCAGCAGCTGCTGCGGAGGAA 7893  
 OY 308 CCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367  
 DB 7894 CCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7953  
 OY 368 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427  
 DB 7954 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8013  
 OY 428 TGGCAAAAATGAGTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487  
 DB 8014 TGGCAAAAATGAGTGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8073  
 OY 488 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547  
 DB 8074 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8133  
 OY 548 TTTTCATCTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607  
 DB 8134 TTTTCATCTCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8193  
 OY 608 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667  
 DB 8194 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8253  
 OY 668 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727  
 DB 8334 AGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8393  
 OY 728 TTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787  
 DB 8314 TTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8373  
 OY 788 GCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8433  
 DB 8374 GCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8493

## Key

Location/Qualifiers

342..2974

/tag= a

W0904008-A2.

28-JAN-1999.

16-JUL-1998; 98W-US014698.

18-JUL-1997; 97US-0053062P.

27-JAN-1998; 98US-00014116.

(US) US DEPT HEALTH &amp; HUMAN SERVICES.

Yangi M, Buxh J, Emerson SU, Purcell RH;

WPI; 1999-132252/11.

P-RSD; AAW98022.

New isolated hepatitis C virus nucleic acids - used to develop products

for the diagnosis, prevention and treatment of HCV infections and for

developing screening assays.

Claim 3; Fig 14a-P; 126pp; English.

The present sequence comprises the nucleic acid sequence of the genome of

infectious hepatitis C virus (HCV) genotype 1b strain HC-J4 (ATCC 209596)

which was obtained from a culture plate plasma of a chimpanzee experimentally

infected with serum containing HC-J4/91. The claimed infectious nucleic

acid sequence can be used to produce infectious nucleic acids (see AAK214833)

consisting of the open reading frames of infectious nucleic acid

sequences of chimpanzee origin (see AAK214833) and of HCV sequences (such

as 1b, 2a, 2b, 3c, 3a, 4a, 4b, 5a and 6a) of HCV. The invention also

relates to the introduction of mutations or deletions into infectious

nucleic acid sequences in order to produce an attenuated HCV virus







XX 03-JUN-2004.  
 XX 13-NOV-2002; 2003WO-EP012793.  
 XX 15-NOV-2002; 2002GB-00026722.  
 XX (GLAX) I GLAXO GROUP LTD.  
 XX Brett S, Hamblin PA, Ogilvie L;  
 XX WPI, 2004-420613/39.  
 XX P-PSDB; A0016227.  
 XX New Hepatitis C virus (HCV) vaccine having a polynucleotide that encodes  
 XX the polypeptide sequences of the HCV core and at least one other HCV  
 XX protein in medicine, particularly for manufacturing a medicament  
 XX for treating HCV.  
 XX Disclosure; Fig 1; 78pp; English.  
 XX The invention describes a polynucleotide vaccine comprising a  
 XX polynucleotide sequence (S1) encoding the Hepatitis C virus (HCV) Core  
 XX protein and at least 1 other HCV protein, and causes expression of the  
 XX proteins in cells (in which (S1) has been mutated or positioned relative  
 XX to the polynucleotide sequence encoding the HCV Core protein, such  
 XX that expression of Core causes over expression of the other HCV  
 XX protein is reduced). Also described are: a method of preventing or  
 XX treating an HCV infection in a mammal, comprising administering the  
 XX vaccine cited above to a mammal; and a method of vaccination of an  
 XX animal, comprising administering the vaccine cited above to an animal,  
 XX coating the polynucleotide onto gold beads and delivering the gold beads  
 XX into the skin. HCV nucleic acids, polypeptides, host cells, vectors and  
 XX antibodies used in the methods, are also disclosed. The polynucleotide  
 XX vaccine is useful in the manufacture of a medicament for the treatment of  
 XX HCV. This sequence encodes the wild type HCV polyprotein.

XX Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 U; 0 Other;

Query Match  
 Matched 1664; Conservative 9.4%; Score 1596.2; DB 12; Length 9595;  
 0; Mismatches 113; Indels 0; Gaps 0;

7594 B GCATCTCAATGCTCTATACATGACAGAGGGGCGCTTATCATCACTGCTCTCGAGGAAA 67  
 DB 57CTCGATATGCTCTATACATGACAGAGGGGCGCTTATCATCACTGCTCTCGAGGAAA 7653

QY 68 SCACAGCTGCATATACCGCTCTGACCAACTCTCTCTGCTGCATCACTPACTGGTCTATT 127  
 DB 68SCACAGCTGCATATACCGCTCTGACCAACTCTCTCTGCTGCATCACTPACTGGTCTATT 127

QY 7654 GTAACTTGCCTCACTCAACCTTGAGCAATCTTCTCTGGTCAACACATCGGTATAG 7713  
 DB 7654GTAACTTGCCTCACTCAACCTTGAGCAATCTTCTCTGGTCAACACATCGGTATAG 7713

QY 128 CCAATCATCCGACATGCGACGACCTCGCGCAGAGAGAGGTCACTTGCAGACTGCAAG 187  
 DB 128CCAATCATCCGACATGCGACGACCTCGCGCAGAGAGAGGTCACTTGCAGACTGCAAG 187

QY 7714 CCAACATATCCGACAGGCAAGCTCTCGCGAGAGAGAGTCACTTGCAGACTGCAAG 7773  
 DB 7714CCAACATATCCGACAGGCAAGCTCTCGCGAGAGAGAGTCACTTGCAGACTGCAAG 7773

QY 188 TCTTGGAGATCAATACCGGAGGTGCTCTAGAGACATGAGAGGAGGTCCACAGTGA 247  
 DB 17774 TCTTGGAGATCAATACCGGAGGTGCTCTAGAGACATGAGAGGAGGTCCACAGTGA 7833

QY 248 AGCGTAACTGCTATCTTGGAGAGCAATGCAAGATGAGAGCGCCCGCATTCACAGTTA 307  
 DB 248AGCGTAACTGCTATCTTGGAGAGCAATGCAAGATGAGAGCGCCCGCATTCACAGTTA 307

QY 7834 AGGCTTAACTGCTATCTTGGAGAGCAATGCAAGATGAGAGCGCCCGCATTCACAGTTA 7893  
 DB 7834AGGCTTAACTGCTATCTTGGAGAGCAATGCAAGATGAGAGCGCCCGCATTCACAGTTA 7893

QY 308 CCAATTTGGCTATGCGGAGAGAGAGGTCTGCGAGGAGGTATGCGAGGCTTTAACCA 367  
 DB 308CCAATTTGGCTATGCGGAGAGAGAGGTCTGCGAGGAGGTATGCGAGGCTTTAACCA 367

QY 7894 CCAATTTGGCTATGCGGAGAGAGAGGTCTGCGAGGAGGTATGCGAGGCTTTAACCA 7953  
 DB 7894CCAATTTGGCTATGCGGAGAGAGAGGTCTGCGAGGAGGTATGCGAGGCTTTAACCA 7953

QY 368 TCGGCTCTGTGTGGAAGATTTCTTGTGCGAGAGAGAGGTCTGCGAGGAGGTATGCGAG 427  
 DB 368TCGGCTCTGTGTGGAAGATTTCTTGTGCGAGAGAGAGGTCTGCGAGGAGGTATGCGAG 427

QY 7954 TCGGCTCTGTGTGGAAGATTTCTTGTGCGAGAGAGAGGTCTGCGAGGAGGTATGCGAG 8013  
 DB 7954TCGGCTCTGTGTGGAAGATTTCTTGTGCGAGAGAGAGGTCTGCGAGGAGGTATGCGAG 8013

QY 428 TGGCGAAAAATGAGGTGTTCTGGCTCAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 4817  
 DB 428TGGCGAAAAATGAGGTGTTCTGGCTCAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 4817

DB 8014 TGGCGAAAAATGAGGTGTTCTGGCTCAACAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 8073  
 QY 488 TCACTGTATATCCCGAGACTCGAGAGTGGTGTATGCGAGAGAGAGGAGGAGGAGGAGGAGG 547  
 DB 8074 TTAATGTATATCCCGAGACTCGAGAGTGGTGTATGCGAGAGAGAGGAGGAGGAGGAGGAG 8133  
 QY 548 TTTTGTATATCCCGAGACTCGAGAGTGGTGTATGCGAGAGAGAGGAGGAGGAGGAGGAGGAG 607  
 DB 8134 TCTTCAACCTCTCTCGAGGCGCTGTATGAGGCTCTCTCAACGATTTCAATACTCCCGCAGC 8193  
 QY 608 AGGGGTGAGGTCTGTGTATATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667  
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 DB 8254 ATGACACACCGCTGTTTGTATCTGTATGCTGTGTGAGAGATGATCATCTGTGTGAGAGTCAA 727  
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 QY 788 GGCCTATGTGTGGGGGTTCGCATCACTATCCAAAGGCGAGACTGGCGCTATATGCGCGGT 8433  
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 QY 908 CGGCTGCGACTGTGTGAGCTCCCAAGCTCCAGAGCTTCAGAGTGTGCTGTGAGTGTGAGAGC 967  
 DB 8494 CGGCTGCGACTGTGTGAGCTCCCAAGCTCCAGAGCTTCAGAGTGTGCTGTGAGTGTGAGAGC 967  
 QY 968 ACTTGTGCTATGCTGTGAGGCGTGTGCTGACGACTAGCTGGGTGTATACCTCACTGCTACTCTGAGG 1027  
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 QY 1028 TACGAGGAGATGACTAGTACTGTCTGCTCCCTCTTGGGACACGCGCTCCACAGAGATACG 1087  
 DB 8614 TACGAGGAGATGACTAGTACTGTCTGCTCCCTCTTGGGACACGCGCTCCACAGAGATACG 8673  
 QY 1088 ACTTGTGCTATGCTGTGAGGCGTGTGCTGACGACTAGCTGGGTGTATACCTCACTGCTACTCTGAGG 1147  
 DB 8674 ACTTGTGCTATGCTGTGAGGCGTGTGCTGACGACTAGCTGGGTGTATACCTCACTGCTACTCTGAGG 1147

QY 1148 AAGGGGTATACTCTATGCTGACCGCTCCACGCTCCCTCTGCGGGGTGTGTGCGAGAG 1207  
 DB 8734 AAGGGGTATACTCTATGCTGACCGCTCCACGCTCCCTCTGCGGGGTGTGTGCGAGAG 8733

QY 1208 CAGTGTGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 1267  
 DB 8794 CAGTGTGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 8853

QY 1268 TGTGCGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 1327  
 DB 8914 TGTGCGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 8913

QY 1328 TGTGAGAGGCTGT 1387  
 DB 8974 TGTGAGAGGCTGT 8973

QY 1388 TACTTCAATATGTGAGATCTGT 1447  
 DB 9034 TACTTCAATATGTGAGATCTGT 9033

QY 1447 CAGTGTGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 1507  
 DB 9094 CAGTGTGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 9093

QY 1508 TGTGCGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 1567  
 DB 9094 TGTGCGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 9093

QY 1567 TGTGCGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 9153  
 DB 9094 TGTGCGAGCACTCTCAAGTCAACTCTGGCTAGGCAAGATCATATGTATGCGCCCACTT 9153





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using av model

Run on: October 3, 2005, 14:01:52 Search time 1971.21 Seconds  
without alignments  
9793.114 Million cell updates/sec

Title: US-10-712-479-1  
Project score: 1  
Sequence: 1 atgctcagtcagtcagtcg.....ggccatccatccatccatccac 1803

Scoring table: IDENTITY\_NOC Gap10 10.0, Gapex1 1.0

Searched: 74423561 seqs, 3452328358 residues 14885122

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 48 summaries

Database : Published Applications NA.\*

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- 3: /cgn2\_6/ptcdat1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptcdat1/pubpna/US06\_PUBCOMB.seq.\*
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- 26: /cgn2\_6/ptcdat1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	1722	95.5	1740	20	US-10-712-479-3
3	1607.4	89.2	1884	9	US-09-838-386-11
4	1597.8	86.5	1955	20	US-10-432-178-5
5	1597.8	86.5	1955	20	US-10-432-178-5
6	1591.4	88.3	1955	20	US-10-432-178-2
7	1585	87.9	6189	15	US-10-259-275-41

8	1585	87.9	6189	24	US-11-006-313-41
9	1585	87.9	7989	17	US-10-434-842-16
10	1585	87.9	7989	19	US-10-639-150-1
11	1585	87.9	7989	17	US-10-434-842-16
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27	1585	87.9	10690	16	US-10-125-920-1
28	1585	87.9	10690	18	US-10-467-000-3
29	1585	87.9	12305	20	US-10-422-123A-2
30	1585	87.9	12305	20	US-10-422-123A-2
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36	1583.4	87.8	8638	13	US-10-029-907-25
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## ALIGNMENTS

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US-10-712-479-1  
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Sequence 1, Application US/10712479  
GENERAL INFORMATION: US/10712479  
GENERAL INFORMATION: US/10712479  
APPLICANT: Vagi, Yoshihiko  
APPLICANT: Sheets, Michael P.  
APPLICANT: Wells, Peter A.  
APPLICANT: Wells, Peter A.  
APPLICANT: Poorman, Roger A.  
APPLICANT: Eppe, Dennis E.  
TITLE OF INVENTION: A Continuous-Read Assay for the Detection of De Novo HCV RNA Poly  
FILE SEQUENCE: US/10712479  
FILE SEQUENCE: US/10712479  
CURRENT APPLICATION NUMBER: US/10712479  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 7  
SEQ ID NOS: 1-7  
SEQ ID NOS: 1-7  
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TYPE: DNA  
ORGANISM: Hepatitis C virus  
NAME/KEY: CDS  
LOCATION: (1)..(1803)  
OTHER INFORMATION:  
US-10-712-479-1  
Query Match 100.0%; Score 1803; DB 20; Length 1803;  
Query Local Similarity 100.0%; Pred. No. 0;





; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQUENCE: 1884  
 ; LENGTH: 1884  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: misc feature  
 ; OTHER INFORMATION: HTASB polymerase  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1881)  
 US-09-838-386-11

Query Match 89.2%; Score 1607.4; DB 9; Length 1884;  
 Best Local Similarity 94.0%; Pred. No. 0;  
 Matches 1671; Conservative 0; Mismatches 106; Indels 0; Gaps 0;  
 8 GCA TGT CAA GTT CTT CAA TCA TCA GAG GCG CCG TGA TCA CAC CTT GCG TGG CTT GCG GAG GAA A 67  
 104 GCT GCG TCA GTT CTT CAC KCT TCA GAG GCG CCG CCG TGA TCA CAC CTT GCG TGG CTT GCG GAG GAA A 67  
 QY 68 GCA GCG TCA GTT CTT CAC KCT TCA GAG GCG CCG CCG TGA TCA CAC CTT GCG TGG CTT GCG GAG GAA A 127  
 164 GCA CAG TCG CCA TCA CAG CCG TTT GAG CAA CTT TTT GCG TGG CTT CAT CCG CAA TGG TCT ATT 223  
 QY 128 GCA CAG TCG CCA TCA CAG CCG TTT GAG CAA CTT TTT GCG TGG CTT CAT CCG CAA TGG TCT ATT 187  
 224 CCA CAG CCG TCG CCA TCA CAG CCG TTT GAG CAA CTT TTT GCG TGG CTT CAT CCG CAA TGG TCT ATT 283  
 QY 188 TCT CCG AGA CAT CAA TCA CCG AGA TGT GCT CAA GCG AGA TGA GAG AGA TGA AGG GTT CCA CAG TGA 347  
 284 TCT CCG AGA CAT CAA TCA CCG AGA TGT GCT CAA GCG AGA TGA GAG AGA TGA AGG GTT CCA CAG TGA 413  
 QY 248 AGC GTT AAT CTT GCT ATT CTT CCG AGA TGT GCT CAA GCG AGA TGA GAG AGA TGA AGG GTT CCA CAG TGA 307  
 344 AGC GTT AAT CTT GCT ATT CTT CCG AGA TGT GCT CAA GCG AGA TGA GAG AGA TGA AGG GTT CCA CAG TGA 403  
 QY 308 CCA AAT TTT GCG TAT GGG CCA AAG ACG GTT CCG AAG CCG TAT CCA GAG GCG CCG GTT TA CCA CCA 367  
 404 CCA AAT TTT GCG TAT GGG CCA AAG ACG GTT CCG AAG CCG TAT CCA GAG GCG CCG GTT TA CCA CCA 463  
 QY 368 TCG AGT TCG GTT GAG AAG CTT GCG TGA GAG CACT GAG CAG CAA TTT CAG ACA CCA TCA CCA 427  
 464 TCG AGT TCG GTT GAG AAG CTT GCG TGA GAG CACT GAG CAG CAA TTT CAG ACA CCA TCA CCA 523  
 QY 428 TCG AAG AAT TGA GGT TTT TCG GTT CCA CCA CCA AAG AAG GAG CCG CCA ACG AGCT TGG CC 487  
 524 TCG AAG AAT TGA GGT TTT TCG GTT CCA CCA CCA AAG AAG GAG CCG CCA ACG AGCT TGG CC 583  
 QY 488 TCA GAT TCG CCA GAG CAG TGG CTT GCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 547  
 584 TTA TCG TAT TCG CCA GAG CAG TGG CTT GCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 643  
 QY 548 TTT CCA CTT CTT CCA GCG CCG TGA TGG CTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 607  
 644 TTT CCA CTT CTT CCA GCG CCG TGA TGG CTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 703  
 QY 608 AGG GCG GTT CCG GTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC TAT GCG GTT CCG GTT 663  
 704 AGG GCG GTT CCG GTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC TAT GCG GTT CCG GTT 767  
 QY 668 ATG ACG CCG GTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC TAT GCG GTT CCG GTT 727  
 764 ATG ACG CCG GTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC TAT GCG GTT CCG GTT 823  
 QY 728 TTT CCA CTT CTT CCA GCG CCG TGA TGG CTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 787  
 824 TTT CCA CTT CTT CCA GCG CCG TGA TGG CTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 883  
 QY 788 GCG TAT CCG GCG GCG CCG CCG TGA TGG CTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 847  
 884 GCG TAT CCG GCG GCG CCG CCG TGA TGG CTT TCG TAT TCG GAG AAG TGG CTT TAA GCG AGCT TGG CC 943

848 GCG GCG CCG 907  
 DB 944 GCG GCG CCG 1003  
 QY 908 GCG GCG CCG 967  
 1004 GCG GCG CCG 1063  
 QY 1068 ACT TCT GCG TAT CTT GAG GAA GCG GGG AACC CAG AAG AAG CCG GCG GCG AAG CCG TAC GAG TCT 1027  
 1064 ACT TCT GCG TAT CTT GAG GAA GCG GGG AACC CAG AAG AAG CCG GCG GCG AAG CCG TAC GAG TCT 1123  
 DB 1028 TCA CCG AAG CCG TAT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1087  
 1124 TCA CCG AAG CCG TAT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1183  
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 1184 ACT GCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1243  
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 1244 AAG GCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1303  
 QY 1208 CAG CTT GCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1267  
 1304 CAG CTT GCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1363  
 QY 1368 TCG GCG AAG CCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1327  
 1364 TCG GCG AAG CCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1423  
 DB 1328 TCG AAG AAG CCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1387  
 1424 TCG AAG AAG CCG TAT CTT GAG CTT GAG TAT CTT GCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1483  
 QY 1388 TACT CAG CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1447  
 1544 TACT CAG CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1543  
 QY 1448 CAG TCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1507  
 1544 CAG TCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1603  
 DB 1508 TCG GCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1567  
 1604 TCG GCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1663  
 QY 1568 CAG TCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1627  
 1664 CAG TCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1723  
 DB 1628 TCG GCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1687  
 1724 TCG GCG AAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT GAG CCG TAT CTT 1783  
 QY 1688 AAG TAT CAG CCG CCG TAT CTT GAG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1747  
 1784 AAG TAT CAG CCG CCG TAT CTT GAG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1843  
 QY 1748 TCT CCG TAG GCG TAG CCG TAT CTT GAG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1784  
 1844 TCT CCG TAG GCG TAG CCG TAT CTT GAG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG CCG 1880

## RESULT 4

US-10-492-178-5 APPLICATION: US/10492178  
 ; PUBLISHED IN: JPLN US2004024761A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Emili, Emilio A.  
 ; APPLICANT: Kaelow, David C.  
 ; AFFILIANT: Best, Andrew J.

```

/ APPLICANT: Shiver, John W.
/ APPLICANT: Nicolas, Alfredo
/ APPLICANT: Lahm, Arlin
/ APPLICANT: Corzago, Alessandro
/ APPLICANT: Colloca, Stefano
/ TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
/ REFERENCE: ITRO0131P, US/10/492,178
/ CURRENT FILING DATE: 2004-04-01
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR FILING DATE: 2001-10-11
/ NUMBER OF SEQ ID NOS: 17
/ SEQ ID NO 5: FastaSeq For Windows Version 4.0
/ LENGTH: 5955
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ NAME/KEY: CDS
/ LOCATION: (1)...(5955)
/ OTHER INFORMATION: NS CDSa sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(5955)
/ US-10-492-178-5

Query Match      88.6%; Score 1597.8; DB 20; Length 5955;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 1665; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY      8  GCATGTCAATCTTCAATACATGACGAGCGCCCTGTATCAACCGCTGGCGTCCGCGAAG 67
Db      4178  GCTGCTCAATGTCTTACACATGATGACGAGCGCCCTGTATCAACCGCTGGCGAAGAA 4237

QY      68  GCAGCTGCGCCTCAACGCGTCAAGCGATGAGCAATGCTGTGCTGCTGCTGCTGCTGCTGCT 127
Db      4218  GCAGCTGCGCCTCAACGCGTGTAGCAACTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4297

QY      128  CGAACGATCCGCGTGTGAAGCTGCGAAGGAGTCACTTTGACAGCTCGAAG 187
Db      4298  CGAACGATCCGCGTGTGAAGGAGTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4357

QY      188  TCTGTAGCATCATATACGGACATGCTCAAGGAGATGAGGAGCGGCTCCACATGA 247
Db      4358  TCTGTAGCATCATATACGGACATGCTCAAGGAGATGAGGAGCGGCTCCACAGTTA 4417

QY      248  AGCTAAATCTATCTGTGAAGAAGATGCAAGCTGAGCGCGCCCGATCGGCGCAAT 307
Db      4418  AGCTAAATCTATCTGTGTGAAGAAGATGCAAGCTGAGCGCGCCCGATCGGCGCAAT 4477

QY      308  CCAAAATTTGGCTATGGGCAAGAGAGCTCGGAGCTATCCGAGCGAGCTTTACACAA 367
Db      4478  CCAAAATTTGGCTATGGGCAAGAGAGCTCGGAGCTATCCGAGCGAGCTTTACACAA 4537

QY      368  TCGCGCTCTGTGTGAGAGATCTTGTGTGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGT 427
Db      4538  TCGCGCTCTGTGTGTGAGAGATCTTGTGTGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGT 4597

QY      428  TCGCGAAATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 487
Db      4598  TCGCGAAATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4657

QY      488  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547
Db      4658  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4717

QY      548  TTTTCATCTTCTTCAGCGCGTATGGGCTCTCTATACGAGATTCGATCTCTCTCAAGC 607
Db      4718  TTTTCATCTTCTTCAGCGCGTATGGGCTCTCTATACGAGATTCGATCTCTCTCAAGC 4777

/ APPLICANT: Shiver, John W.
/ APPLICANT: Nicolas, Alfredo
/ APPLICANT: Lahm, Arlin
/ APPLICANT: Corzago, Alessandro
/ APPLICANT: Colloca, Stefano
/ TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
/ REFERENCE: ITRO0131P, US/10/492,178
/ CURRENT FILING DATE: 2004-04-01
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR FILING DATE: 2001-10-11
/ NUMBER OF SEQ ID NOS: 17
/ SEQ ID NO 5: FastaSeq For Windows Version 4.0
/ LENGTH: 5955
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ NAME/KEY: CDS
/ LOCATION: (1)...(5955)
/ OTHER INFORMATION: NS CDSa sequence
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(5955)
/ US-10-492-178-5

QY      608  AGCGGCTCGAGTCTCTGTGTGATCTCTGAAAGCAAGAAAATGCCCTATGGGCTCTCAT 667
Db      4778  AGCGGCTCGAGTCTCTGTGTGATCTCTGAAAGCAAGAAAATGCCCTATGGGCTCTCAT 677

QY      668  ATGACACACCGCTCTGTGTGATCTCTACACGCTCACTCAGAAATGATGATCGGTGTGAGAGTCAA 1237
Db      4838  ATGACACACCGCTCTGTGTGATCTCTACACGCTCACTCAGAAATGATGATCGGTGTGAGAGTCAA 1287

QY      728  TTTACCAATGTGTGTGATCTCTGTGTGATCTCTGTGTGATCTCTGTGTGATCTCTGTGTGAT 787
Db      4898  TTTACCAATGTGTGTGATCTCTGTGTGATCTCTGTGTGATCTCTGTGTGATCTCTGTGTGAT 847

QY      788  GGCTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
Db      4958  GGCTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907

QY      848  GCGCGCGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db      5018  GCGCGCGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967

QY      908  GCGCGCGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
Db      5078  GCGCGCGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027

QY      968  AGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027
Db      5138  AGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1087

QY      1028  TACGAGAGCTATGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1087
Db      5198  TACGAGAGCTATGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147

QY      1088  ACTTGTGAGCTGTATTAACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
Db      5258  ACTTGTGAGCTGTATTAACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207

QY      1148  AAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
Db      5318  AAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1267

QY      1208  CAGCTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1267
Db      5378  CAGCTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1327

QY      1268  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1327
Db      5438  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1387

QY      1328  TTTAAAAAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1387
Db      5498  TTTAAAAAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447

QY      1388  TACTCTGAGCTATTAAGCAAGCTCTCATGGCTGTAGGCGCATTTTCTCTCTCATGATGATCTCT 1447
Db      5558  TACTCTGAGCTATTAAGCAAGCTCTCATGGCTGTAGGCGCATTTTCTCTCTCATGATGATCTCT 1507

QY      1448  CAGCTGTGAGCTATTAAGGCGCTTCTCATGGCTGTAGGCGCATTTTCTCTCTCATGATGATCTCT 1507
Db      5618  CAGCTGTGAGCTATTAAGGCGCTTCTCATGGCTGTAGGCGCATTTTCTCTCTCATGATGATCTCT 1567

QY      1508  TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1567
Db      5678  TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1627

QY      1568  CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1627
Db      5738  CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1687

QY      1628  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1687
Db      5798  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747

QY      1688  AONATATACAGAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747

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Db 5318 AAGGGGTGATCTATCTACACCGGTGACCTCACACCCCTCTGGCGGGCTGTGGGAGA 5377  
 Qy 1208 CAGCTTAGGACATCTCAGTCAATCTCTCTAGCGAACATCATATGATGGCCACTT 1267  
 Db 5378 CAGTGAACACATCTCAGTCAATCTCTCTAGCGAACATCATATGATGGCCACTT 5437  
 Qy 1268 TGTGGGACAGATGATCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327  
 Db 5438 TGTGGGACAGATGATCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5497  
 Qy 1328 TGTAAAGAGCTGGATCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1387  
 Db 5498 TGTAAAGAGCTGGATCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5557  
 Qy 1388 TACTCTGATGATCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1447  
 Db 5558 TACTCTGATGATCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5617  
 Qy 1448 CAGTGAATCAATAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1507  
 Db 5618 CAGTGAATCAATAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5677  
 Qy 1508 TCTGAGACATCTGGGCGAAGATGCTCTGGGCTAGTACTGTCTCCCGAGGGGAGGCG 1567  
 Db 5678 TCTGAGACATCTGGGCGAAGATGCTCTGGGCTAGTACTGTCTCCCGAGGGGAGGCG 1627  
 Qy 1568 CAAATTTGGGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1627  
 Db 5738 CAAATTTGGGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5797  
 Qy 1628 TTTCCGGCTGGCTCTGGGCTGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1687  
 Db 5798 TTTCCGGCTGGCTCTGGGCTGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5857  
 Qy 1688 ACATATATACACGCT 1747  
 Db 5858 ACATATATACACGCT 5917  
 Qy 1748 TCTCTGAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 1784  
 Db 5918 TTTCTGTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGG 5954

RESULT 8  
 / Sequence 41, Application US/11006313  
 / Publication No. US20050153281A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Y1, Minkyung M.  
 / TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
 / FILE REFERENCE: 265,0007 0121  
 / CURRENT APPLICATION NUMBER: US/11/006,313  
 / PRIOR APPLICATION NUMBER: US 60/171,909  
 / PRIOR FILING DATE: 1999-12-23  
 / PRIOR APPLICATION NUMBER: US 10/259,275  
 / PRIOR FILING DATE: 2001-09-27  
 / PRIOR APPLICATION NUMBER: US 09/747,419  
 / PRIOR FILING DATE: 2000-12-23  
 / PRIOR APPLICATION NUMBER: US 60/325,236  
 / PRIOR FILING DATE: 2001-09-27  
 / PRIOR APPLICATION NUMBER: US 10/338,123  
 / PRIOR FILING DATE: 2001-11-13  
 / NUMBER OF SEQ ID NOS: 73  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 41  
 / LENGTH: 1839  
 / TYPE: DNA  
 / ORGANISM: ARTIFICIAL  
 / FEATURE:  
 / OTHER INFORMATION: nucleotide sequence encoding hepatitis C virus polypeptide

/ OTHER INFORMATION: derived from Cont  
 / us-11-006-313-41  
 Query Match 87.91; Score 1585; DB 24; Length 6189;  
 Best Local Similarity 93.21; Pred. No. 0;  
 Matches 1657; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
 Qy 8 GGAATGATGATCTCTATATGATGATGATGATGATGATGATGATGATGATGATGATG 67  
 Db 4178 GGTGCTCTGATGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 4237  
 Qy 68 GGAATGATGATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 127  
 Db 4238 GGAATGATGATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 4297  
 Qy 128 CTAATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 187  
 Db 4298 CTAATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4357  
 Qy 188 TCTCTGAGATGATCTCTGAGGATGATGAGGATGAGGATGAGGATGAGGATGAGGATG 247  
 Db 4358 TCTCTGAGATGATCTCTGAGGATGATGAGGATGAGGATGAGGATGAGGATGAGGATG 4417  
 Qy 248 AGCTAAATCTCTATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 307  
 Db 4418 AGCTAAATCTCTATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 4477  
 Qy 308 CCAATTTGGCTATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 367  
 Db 4478 CCAATTTGGCTATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 4537  
 Qy 368 TCGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 427  
 Db 4538 TCGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4597  
 Qy 428 TGGCAAAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 487  
 Db 4598 TGGCAAAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 4657  
 Qy 488 TCAATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 547  
 Db 4658 TCAATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5717  
 Qy 548 TTTCAATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 607  
 Db 4718 TTTCAATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4777  
 Qy 608 AGCGGTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 667  
 Db 4778 AGCGGTCTGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4837  
 Qy 668 ATGACACCGCTCTTGGATCTCAACGCTCACTGATGATGATGATGATGATGATGATG 727  
 Db 4838 ATGACACCGCTCTTGGATCTCAACGCTCACTGATGATGATGATGATGATGATGATG 4897  
 Qy 728 TTTACACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 787  
 Db 4898 TTTACACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4957  
 Qy 788 GCGCTATCTGCGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 847  
 Db 4958 GCGCTATCTGCGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5017  
 Qy 848 GCGCGCGGCGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 907  
 Db 5018 GCGCGCGGCGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5077  
 Qy 908 CCGCTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 967  
 Db 5078 CCGCTGACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5137  
 Qy 968 ACCTTCTGCTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1027



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Db 6875 CCGTGGCGCTCTCGAGTCTCGAGCTCGAGCTCGAGCTCTCTATGCGGAGAG 6934
Qy 968 ACTTGTGTGTATCTGTGAAGCGCGGAGCCCAAGAGAGAGCGGAGCTAGAGTCT 1027
Db 6935 ACTTGTGTGTATCTGTGAAGCGCGGAGCCCAAGAGAGAGCGGAGCTAGAGTCT 6994
Qy 1028 TCAGCGAGCTAGTACGAGTCTGTGAGTCTGTGAGTCTGTGAGTCTGTGAGTCT 1097
Db 6995 TCAGCGAGCTAGTACGAGTCTGTGAGTCTGTGAGTCTGTGAGTCTGTGAGTCT 7054
Qy 1088 ACTTGGAGCTGTATACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
Db 7055 ACTTGGAGCTGTATACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7114
Qy 1148 AATGGGTGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1207
Db 7115 AATGGGTGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7174
Qy 1208 CAGTATAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1267
Db 7175 CAGTATAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7234
Qy 1268 TGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327
Db 7235 TGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7294
Qy 1328 TTGAAAAGCTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1387
Db 7295 TTGAAAAGCTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7354
Qy 1388 TACTCTAGATCTATGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1447
Db 7355 TACTCTAGATCTATGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7414
Qy 1448 CAGTATAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1507
Db 7415 CAGTATAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1567
Qy 1508 TGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1567
Db 7475 TGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7534
Qy 1568 CACTTGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1627
Db 7535 CACTTGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7594
Qy 1628 TGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1687
Db 7595 TGTGGCGAGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7654
Qy 1688 ACATATATACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1747
Db 7655 ACATATATACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7714
Qy 1748 TCTCTGTATGGGTGTAGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1784
Db 7715 TCTCTGTATGGGTGTAGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7751

```

## RESULT 10

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US-10-639-150-1
; Sequence 1: Application US/10639150
; Submission No. US20040121975A1
; Applicant: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: HEPATITIS C VIRUS ASSAYS
; FILE REFERENCE: D0324 NP
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 40/402,461
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 5

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HCV Replicon
US-10-639-150-1

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Query Match      87.94; Score 1585; DB 19; Length 7989;
Best Local Similarity 93.24; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
Qy 8 GAATGTCAATGTCTCTATCATGAGGAGCGCCCTGATCACGCTGCGTGGGAGGAAA 67
Db 5978 GGTGCTCGCATCTCTCTACCATGAGCGCCCTGATCACGCTGCGTGGGAGGAAA 6037
Qy 67 68 GGTGCTCGCATCTCTCTACCATGAGCGCCCTGATCACGCTGCGTGGGAGGAAA 1297
Db 6038 CGAAGCTGCCCATCAATGCAATGCAATCTTCTGCTGATCACCAATCTGCTCTATG 1497
Qy 128 CCAATCTCTGCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 187
Db 6098 CTACAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6157
Qy 188 TCTCTGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 247
Db 6158 TCTCTGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6217
Qy 248 AGCTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 307
Db 6218 AGCTAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6277
Qy 308 CCAATTTGGCTCTATGCGGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
Db 6278 CTAAATTTGGCTCTATGCGGCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCT 6337
Qy 368 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
Db 6338 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6397
Qy 428 TGGCAAAATATGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 487
Db 6398 TGGCAAAATATGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4457
Qy 448 TCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 547
Db 6458 TTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6517
Qy 548 TTTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 607
Db 6518 TCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6577
Qy 608 AGCGGTGCGATCTCTCTGTAATCTCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 667
Db 6578 AGCGGTGCGATCTCTCTGTAATCTCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 6637
Qy 668 ATGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 727
Db 6638 ATGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6697
Qy 728 TTTTCAATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 787
Db 6698 TTTTCAATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6757
Qy 788 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 847
Db 6758 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6817
Qy 848 GCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 907
Db 6818 GCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6877

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Qy 848 GCGCGCGCGCGCGCGCTGACACACACCTGCGTAATACCTCAATCTACTCTGAGG 907
Db GCGCGCGCGCGCGCGCTGACACACACCTGCGTAATACCTCAATCTACTCTGAGG 907
Qy 908 CCGCTCGAGCGCTGTGAGCTGCCAAGCTCAGAGCTGCAAGTCTGTGAATGAGAGG 967
Db CCGCTCGAGCGCTGTGAGCTGCCAAGCTCAGAGCTGCAAGTCTGTGAATGAGAGG 967
Qy 6878 CCGCTCGAGCGCTGTGAGCTGCCAAGCTCAGAGCTGCAAGTCTGTGAATGAGAGG 6937
Db CCGCTCGAGCGCTGTGAGCTGCCAAGCTCAGAGCTGCAAGTCTGTGAATGAGAGG 6937
Qy 968 ACTCTGTGTTATCTGTGAAGCGCGGCAACCAAGAGAGCGCGCAAGCTCAAGTCT 1027
Db ACTCTGTGTTATCTGTGAAGCGCGGCAACCAAGAGAGCGCGCAAGCTCAAGTCT 1027
Qy 6938 ACTCTGTGTTATCTGTGAAGCGCGGCAACCAAGAGAGCGCGCAAGCTCAAGTCT 6997
Db ACTCTGTGTTATCTGTGAAGCGCGGCAACCAAGAGAGCGCGCAAGCTCAAGTCT 6997
Qy 6998 TCACGAGGAGTATGATAGCTATGCTGCGCCCGCTGGAGACAGCGCGCAAGTCTAC 1087
Db TCACGAGGAGTATGATAGCTATGCTGCGCCCGCTGGAGACAGCGCGCAAGTCTAC 1087
Qy 1088 ACTCTGAGCTATGATATGCTGCTGCAAGTCTGCGCGCGCGCAAGTCTACGCGCA 1147
Db ACTCTGAGCTATGATATGCTGCTGCAAGTCTGCGCGCGCGCAAGTCTACGCGCA 1147
Qy 7058 ACTTGAAGTATGATATGATATGCTGCTGCAAGTCTGCGCGCGCGCAAGTCTAC 7117
Db ACTTGAAGTATGATATGATATGCTGCTGCAAGTCTGCGCGCGCGCAAGTCTAC 7117
Qy 1148 AAGAGGTTATGATATGATATGCTGCTGCAAGTCTGCGCGCGCGCAAGTCTAC 1207
Db AAGAGGTTATGATATGATATGCTGCTGCAAGTCTGCGCGCGCGCAAGTCTAC 1207
Qy 1208 CAGCTGAGCGACATCTGAGTGAATCTGCTGCTGAGCAAAATATATATATGCGCACT 1267
Db CAGCTGAGCGACATCTGAGTGAATCTGCTGCTGAGCAAAATATATATATGCGCACT 1267
Qy 7178 CAGCTGAGCGACATCTGAGTGAATCTGCTGCTGAGCAAAATATATATATGCGCACT 7237
Db CAGCTGAGCGACATCTGAGTGAATCTGCTGCTGAGCAAAATATATATATGCGCACT 7237
Qy 1268 TGTGCGCAGATGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1327
Db TGTGCGCAGATGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1327
Qy 7238 TGTGCGCAGATGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7297
Db TGTGCGCAGATGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7297
Qy 1328 TTGAAAAGCGCTTGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1387
Db TTGAAAAGCGCTTGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1387
Qy 7298 TTGAAAAGCGCTTGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7357
Db TTGAAAAGCGCTTGATATGATATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7357
Qy 1388 TACCTCAGATCATGATGACGATCATGATGCTTATAGCGCATTTTCACTCCATGATCTCTC 1447
Db TACCTCAGATCATGATGACGATCATGATGCTTATAGCGCATTTTCACTCCATGATCTCTC 1447
Qy 7358 TACCTCAGATCATGATGACGATCATGATGCTTATAGCGCATTTTCACTCCATGATCTCTC 7417
Db TACCTCAGATCATGATGACGATCATGATGCTTATAGCGCATTTTCACTCCATGATCTCTC 7417
Qy 1448 CAGCTGAGCTATGATGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1507
Db CAGCTGAGCTATGATGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1507
Qy 7418 CAGCTGAGCTATGATGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7477
Db CAGCTGAGCTATGATGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7477
Qy 1508 TCTGAGAGCTGCGCGCAAGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1567
Db TCTGAGAGCTGCGCGCAAGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 1567
Qy 7478 TCTGAGAGCTGCGCGCAAGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7537
Db TCTGAGAGCTGCGCGCAAGATGCTGCTGCTGAGCAAAATATATATATGCGCACT 7537
Qy 1568 CAAATTTGCGAGATGATCTCTTCACTGCGCGATGAGCAAAATATATATATGCGCACT 1627
Db CAAATTTGCGAGATGATCTCTTCACTGCGCGATGAGCAAAATATATATATGCGCACT 1627
Qy 7538 CAAATTTGCGAGATGATCTCTTCACTGCGCGATGAGCAAAATATATATATGCGCACT 7597
Db CAAATTTGCGAGATGATCTCTTCACTGCGCGATGAGCAAAATATATATATGCGCACT 7597
Qy 1628 TCTGCGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1687
Db TCTGCGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1687
Qy 7598 TCTGCGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 7657
Db TCTGCGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 7657
Qy 1688 ACAAATATGACAGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGAT 1747
Db ACAAATATGACAGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGAT 1747
Qy 7658 ACAAATATGACAGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGAT 7717
Db ACAAATATGACAGCTGCTGCTGCGCGATGATGATGATGATGATGATGATGATGAT 7717
Qy 1748 TCTGCTGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1784
Db TCTGCTGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1784
Qy 7718 TTTCTGTAAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7754
Db TTTCTGTAAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7754

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## RESULT 14

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US-10-005-469-4
; Sequence 4, Application US/10005469
; Publication No. US2005015513A1
; APPLICANT: ANADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RBH

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; FILE REFERENCE: 0342/IH95U81
; CURRENT APPLICATION NUMBER: US/10/005,469
; PUBLICATION NUMBER: US2005015513A1
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.1
; SOURCE: Synthetic
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; DESCRIPTION: HCV Replicon RNA from cell line HCVp9
; COMMENT:
US-10-005-469-4

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## Query Match

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; Accession: 87.98; Score 1585; DB 13; Length 7992;
; Description: Similarity 93.2%; Pred. No. 0;
; Match: 1657; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

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Qy 8 GCATGTCAATGCTCTATCATGACAGCGCCCTGTATCATCATCGTGGCTGCGAGAAA 67
Db 5978 GCTCTCAATGCTCTATCATGACAGCGCCCTGTATCATCATCGTGGCTGCGAGAAA 6037
Qy 68 GGAAGTGTCCCATCAACCGCTGTAGCAACTCTCTGTGTGTCACCATTAACCTGTATT 127
Db 6038 CGAAGTGTCCCATCAACCGCTGTAGCAACTCTCTGTGTGTCACCATTAACCTGTATT 127
Qy 128 CCAAGTGTCCCATCAACCGCTGTAGCAACTCTCTGTGTGTCACCATTAACCTGTATT 687
Db 6038 CCAAGTGTCCCATCAACCGCTGTAGCAACTCTCTGTGTGTCACCATTAACCTGTATT 687
Qy 6098 CTAAACATCTCCGAGCGCAACCTCTCCGCGAAGAGAGTCACTTTTACAGATCGAGG 6157
Db 6098 CTAAACATCTCCGAGCGCAACCTCTCCGCGAAGAGAGTCACTTTTACAGATCGAGG 6157
Qy 188 TCCTCGAGCATCAATACGCGATCTGTCTGATGAGATGATGAGGAGGAGGCTCGACATGA 247
Db 6158 TCCTCGAGCATCAATACGCGATCTGTCTGATGAGATGATGAGGAGGAGGCTCGACATGA 247
Qy 248 AGCTAAATCTCTATCTAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 307
Db 6218 AGCTAAATCTCTATCTAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 307
Qy 308 CCAATTTGCTATGCGCGAAGAGAGCTCGAGAGCTTATCATGAGAGGCGTTAACGACA 367
Db 6278 CTAATTTGCTATGCGCGAAGAGAGCTTATCATGAGAGGCGTTAACGACA 367
Qy 368 TCCTGCTGTGTGAGAGATCTGTGTGAGAGCATGACACACACCATTTGACACACATCA 427
Db 6318 TCCTGCTGTGTGAGAGATCTGTGTGAGAGCATGACACACACCATTTGACACACATCA 427
Qy 428 TCGCAAAAATAGAGTGTTCCTGCTCCACAGACAGAGAGAGGCGCGAACCAAGCTGCC 437
Db 6398 TCGCAAAAATAGAGTGTTCCTGCTCCACAGACAGAGAGAGGCGCGAACCAAGCTGCC 437
Qy 488 TCAATGATATCCCACTCTGAGGATCTGTGATGCGAGAGATGGCCCTTTACAGATGG 547
Db 6458 TCAATGATATCCCACTCTGAGGATCTGTGATGCGAGAGATGGCCCTTTACAGATGG 547
Qy 548 TTTCACCTCTCTAGCGGCTGTAGGAGCTCTCTATACGAGATTCGATCTCTCTAGC 607
Db 6518 TTTCACCTCTCTAGCGGCTGTAGGAGCTCTCTATACGAGATTCGATCTCTCTAGC 607
Qy 608 AGCGGCGAGTCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 657
Db 6578 AGCGGCGAGTCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 657
Qy 668 ATGACACCGCTGTTTGAATCTCAAGGCTCACTGTGAGATGATGATGATGATGATGAT 727
Db 6638 ATGACACCGCTGTTTGAATCTCAAGGCTCACTGTGAGATGATGATGATGATGATGAT 727
Qy 728 TTATCAATGCTGTGATCTTGGCCCGAGAGCTAGACAGGCGATAAGTGTCTCAGACAG 787
Db 6698 TTATCAATGCTGTGATCTTGGCCCGAGAGCTAGACAGGCGATAAGTGTCTCAGACAG 787
Qy 788 GGCTCTATGTGGGGGTCCCATGATCACTCCAAAGGCGAAGATCGCGGCTTATCGCGGT 847
Db 788 GGCTCTATGTGGGGGTCCCATGATCACTCCAAAGGCGAAGATCGCGGCTTATCGCGGT 847

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Db 6758 GCGTTTACAGTCGGGGGCCCTGACTTCTTAAAGGCGAGACCTCGCGCTATCGCGGT 6817  
 Oy 848 CCGCGCGGAGCGGGCTGTGACAGCATAGTCGGGTAACTACCTCACATCTACTTGAAGG 907  
 Db 6818 CCGCGCGGAGCGGGTGTATACGACGAGCTCGCGGTAACTACCTCATATCTACTTGAAGG 6877  
 Oy 908 CCGCGCGGAGCTCTCAAGCTCGAGCTCGCGGTAACTACCTCAATCTACTTGAAGG 967  
 Db 6878 CCGCGCGGAGCTCTCAAGCTCGAGCTCGCGGTAACTACCTCAATCTACTTGAAGG 6937  
 Oy 968 ACCTGTGTGTATCTGTGAGAGCGGGGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027  
 Db 6938 ACCTGTGTGTATCTGTGAGAGCGGGGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 6997  
 Oy 1028 TCAAG 1087  
 Db 1088 ACTTGGAGCTGTATACATCTGTCTCTCATATCTGTCTCATATCTGTCTCATATCTGTCT 1147  
 Db 7058 ACTTGGAGCTGTATACATCTGTCTCTCATATCTGTCTCATATCTGTCTCATATCTGTCT 7117  
 Oy 1148 AAG 1207  
 Db 7118 AAG 7177  
 Oy 1208 GAGCTAGGAG 1267  
 Db 7178 GAGCTAGGAG 7237  
 Oy 1268 TGTGCGGAG 1327  
 Db 7238 TGTGCGGAG 1387  
 Oy 1328 TGTGCGGAG 1387  
 Db 7298 TGTGCGGAG 7357  
 Oy 1388 TACTGTGAG 1447  
 Db 7358 TACTGTGAG 7417  
 Oy 1448 CAGGTGAG 1507  
 Db 7418 CAGGTGAG 7477  
 Oy 1508 TCTGCGGAG 1567  
 Db 7478 TCTGCGGAG 7537  
 Oy 1568 CAGGTGAG 1627  
 Db 7538 CAGGTGAG 7597  
 Oy 1628 TCTGCGGAG 1687  
 Db 7598 TCTGCGGAG 7657  
 Oy 1688 ACTGATGAG 1747  
 Db 7658 ACTGATGAG 7717  
 Oy 1748 TCTGCGGAG 1784  
 Db 7718 TCTGCGGAG 7754

## RESULT 15

US-10-005-469-5

; Sequence 5, Application US/10005469

; Publication No. US20020155133A1

; GENERAL INFORMATION

; APPLICANT: ANDRUS Pharmaceuticals, Inc.

; APPLICANT: Biobio, Vadim  
 ; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFIC  
 ; FILE REFERENCE: 0342/1H95N81  
 ; CURRENT APPLICATION NUMBER: US/10/005,469  
 ; PRIOR FILING DATE: 2002-04-18  
 ; PRIOR FILING DATE: 2000-11-07  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 5 992  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HCV Replicon from cell line HCV22  
 US-10-005-469-5

Query Match 87.94; Score 1585; DB 13; Length 7992;

Best Local Similarity 93.24; Pred. No. 0; Gaps 0;  
 Matches 1457; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
 Oy 8 GCATGTCTCATGTCTATATCATGACAGAGCGGCGCTGATCATGACGTGGTCCGAGGAAA 67  
 Db 5978 GCTCTCTCATGTCTATACNCACTGAGAGCGGCGCTATGATGCGTCTGCGGAGAAA 6037  
 Oy 68 GCAGAGTCCCATCAAGCGGCTGAGACATCTCTGTGCTGTCGTCACATAACCTGGTCTATT 127  
 Db 6038 CAGAGTCCCATCAAGCTGATGACATCTCTGTGCTGTCGTCACATAACCTGGTCTATT 6097  
 Oy 128 CAGAGTCCCATCAAGCTGATGACATCTCTGTGCTGTCGTCACATAACCTGGTCTATT 187  
 Db 6098 CTAACACATCTCGAGAGGAGAGCTGCGGCAAGAGAGTCACTTTGACAGATCTGAGG 6157  
 Oy 188 TCTGTGACATCATATACGAGAGAGTCTGACAGAGATGAGAGAGAGAGAGAGAGAGAG 247  
 Db 6158 TCTGTGACAGAGCTACAGCGAGAGTCTGACAGAGATGAGAGAGAGAGAGAGAGAGAG 6217  
 Oy 248 AGGCTAAATCTGATATCTGTAGAGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 307  
 Db 6218 AGGCTAAATCTGATATCTGTAGAGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 6277  
 Oy 308 CAAATTTTGGCTATGGGGGAAAGAGAGCTCGAGAGCTTATCGAGAGGCGCTTATACACA 367  
 Db 6278 CTAAATTTTGGCTATGGGGGAAAGAGAGCTCGAGAGCTTATCGAGAGGCGCTTATACACA 6337  
 Oy 368 TCGGCTCGGTGTGAGAGAGCTTCTGTGAGAGACATCGACACCAATTCAGACACATCTCA 428  
 Db 6338 TCGGCTCGGTGTGAGAGAGCTTCTGTGAGAGACATCGACACCAATTCAGACACATCTCA 4397  
 Oy 428 TGGCAAAAATAGAGTTTCTGTGCTCCACAGAGAAAGAGAGCGGCAACAGAGCTGCC 457  
 Db 6398 TGGCAAAAATAGAGTTTCTGTGCTCCACAGAGAAAGAGAGCGGCAACAGAGCTGCC 6457  
 Oy 488 TCACTGATATCCAGAGCTGGAGTGGATATCCAGAGAGAGAGAGAGAGAGAGAGAGAG 547  
 Db 6458 TTAATCTATCCAGAGCTGGAGTGGATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6517  
 Oy 548 TTTCATCTGTCTGAG 607  
 Db 6518 TCTCAACCTCTCTGAG 6577  
 Oy 608 AGGCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT 6637  
 Db 6578 AGGCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT 6637  
 Oy 668 ATGACAG 727  
 Db 6638 ATGACAG 6697  
 Oy 728 TTATACCAATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT 787  
 Db 6698 TCTACCAATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCTGATATCT 6757



***This Page Blank (uspto)***



; MOLECULE TYPE: DNA

; FEATURE: OTHER INFORMATION: K101-18C1, FIG. 2

; SEQUENCE DESCRIPTION: SEQ ID NO: 95

US-08-150-204E-95

Query Match 85.24; Score 1607.4; DB 4; Length 9472;  
 Percent Identity 91.01; Pos 95  
 Matrix 1671; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy B CCAATGTAATGCTCTATPACATCGACAGCGCGCTGTATCAACCTCGCTCGCGAGAAA 67  
 Db 7595 GCTGTGTAATGCTCTATPACATCGACAGCGCGCTGTATCAACCTCGCTCGCGAGAAA 7654  
 Qy 68 CCAAGCTGCTCAATCAAGCGCTGAGCAACTCTCTGCTGCATCAATCACTGGCTATT 127  
 Db 7655 CCAAGCTGCTCAATCAAGCGCTGAGCAACTCTCTGCTGCATCAATCACTGGCTATT 134  
 Qy 128 CACACATATCCGACATGAGCTCTGGCGAGAGAGAGTCACTCTGACAGATGCAAG 177  
 Db 7715 CACACATATCCGACATGAGCTCTGGCGAGAGAGAGTCACTCTGACAGATGCAAG 1774  
 Qy 188 CACAGAGATCAATCAAGCGCTGCTCTGAGAGATGAGCGAGAGGCTCCACAGTGA 247  
 Db 7775 CACAGAGATCAATCAAGCGCTGCTCTGAGAGATGAGCGAGAGGCTCCACAGTGA 247  
 Qy 248 AGCTGATGCTGATCTCTGAGAGAGAGAGTGAAGTGAAGTGGAGTGGCGAGTGC 307  
 Db 7835 AGCTGATGCTGATCTCTGAGAGAGAGAGTGAAGTGAAGTGGAGTGGCGAGTGC 307  
 Qy 308 CCAATTTGCTATGGCGAAGGAGCTGCGAGGCTATTCACAGAGGCGGTATACACA 367  
 Db 7895 CCAATTTGCTATGGCGAAGGAGCTGCGAGGCTATTCACAGAGGCGGTATACACA 367  
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 Db 7955 TCGCTCTGCTGTGAGAGATCTGTGAGAGAGCACTGACACCAATTCACAGACATCA 427  
 Qy 428 TCGCAAAATAGAGGTTTTCTGGGTCCACAGAGAGAGAGGCGCAACACAGCTGCC 487  
 Db 8015 TCGCAAAATAGAGGTTTTCTGGGTCCACAGAGAGAGAGGCGCAACACAGCTGCC 487  
 Qy 468 TCATGATGTCACAGACTCGGAGTTTGTGTATGCGAGAGATGGCGCTTACAGCTGG 547  
 Db 8075 TCATGATGTCACAGACTCGGAGTTTGTGTATGCGAGAGATGGCGCTTACAGCTGG 547  
 Qy 548 TTATGCTGCTCTCTGAGCGCTGATGGGCTCTCTATGCGGATTCATGCTTCAAGC 617  
 Db 8135 TTATGCTGCTCTCTGAGCGCTGATGGGCTCTCTATGCGGATTCATGCTTCAAGC 617  
 Qy 608 AGCGGTGGATGCTCTGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667  
 Db 8195 AGCGGTGGATGCTCTGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667  
 Qy 668 ATGACATCGCTGTTTATCAATCAAGTATCTGAGATATGATATGATATGATATGAT 727  
 Db 8254 ATGACATCGCTGTTTATCAATCAAGTATCTGAGATATGATATGATATGATATGAT 727  
 Qy 8315 ATGACATCGCTGTTTATCAATCAAGTATCTGAGATATGATATGATATGATATGAT 8314  
 Db 8315 ATGACATCGCTGTTTATCAATCAAGTATCTGAGATATGATATGATATGATATGAT 8314  
 Qy 728 TTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 787  
 Db 8315 TTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8314  
 Qy 788 GGTCTCTATGCTGGGGGTCCTATGATTAATCTCAAGAGCGAGATCGGCTATCGCGGT 847  
 Db 8375 GGTCTCTATGCTGGGGGTCCTATGATTAATCTCAAGAGCGAGATCGGCTATCGCGGT 847  
 Qy 848 GCGCGCGAGAGCGGGTGTCCAGAGCTAGCTGGGTATATACCTCAATGCTACTGAGG 907  
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 Qy 1568 CCAATTTGGGCAAGTACTCTCTTCACTTGGGCAATGAGACAGCTTAACTCATCTCA 1627  
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 Db 9335 TCTCGTGAAGGTAGGATCACTATCACTACTCCCAACCG 9371

## RESULT 2

4-416-4

US Patent No. 6,153,421

Sequence 4, Application US/09014416

Patent No. 6,153,421

GENERAL INFORMATION:

APPLICANT: Masayuki, Masayuki

APPLICANT: Masayuki, Masayuki

APPLICANT: Masayuki, Masayuki

TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND



NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amstrong, Westernman, Hattori, McElmold &  
 ATTORNEYS: 1725 K St. N.W. Suite 1000  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 in. 1.44MB  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/324,977  
 FILING DATE: 18-OCT-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-167466  
 FILING DATE: 25-JUN-1990

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-210921  
 FILING DATE: 25-JUN-1990

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-105605  
 FILING DATE: 09-NOV-1990

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/099,706  
 FILING DATE: 30-JUL-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/635,451  
 FILING DATE: 28-DEC-1990

ATTORNEY/AGENT INFORMATION:  
 NAME: Strenuous, Hattori, McElmold &  
 REFERENCE/DOCKET NUMBER: 900703D

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 459-2930  
 TELEFAX: (202) 459-0357

INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2991 base pairs  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA from genomic RNA

FEATURE KEY: misc feature  
 LOCATION: 1..2991

OTHER INFORMATION: /note: "sequence = 6372 - 9362 of  
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FEATURE KEY: CDS  
 LOCATION: 1..2991

US-08-324-977-49

Query March 88.48; Score 1583; DB 1; Length 2991;  
 Basic Local Similarity 93.58; Pred. No. 0;  
 Marches 1662; Conservative

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 QY 188 TCTCTCGACGATCATTAACCGGCGATCTCCAGGAGGAGGAGGAGGCTCCACAGTGA 247  
 DB 1394 TCTTGGACGACCTACCGGAGGTCTCAGGAGAGTGAAGGCGAGGCGTCCAGATTGA 1453  
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 DB 1454 AGGCTTAATCTCTATCTGTATAGAGAGCATGCGCAAGCTGACGCCGCCCATTTGGGCCAAT 1513  
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 QY 488 TCACTGATATCCGAGAGCTGGAGGCTGTGTATGAGAGAGAGTGGCTTTTATGAGTGG 547  
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 QY 668 ATGACACCGCTGTGTGACTCAAGCTCTACTGAGAGTGAATCTCTGAGAGTGAAT 727  
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 QY 847 GGTCTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847  
 DB 1994 GGTCTATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2053  
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 QY 908 CGGCTGCGAGCTGTGAGCTTCCAGGCTCGAGAGCTGAGAGCTCTGTGTAATGAGAG 2113  
 DB 2114 CTTCTGAGCTGTGAGCTTCCAGGCTCGAGAGCTGAGAGCTCTGTGTAATGAGAG 2173  
 QY 968 ACCTTGTGTTATCTGGAAGCGGAGAACCAAGAGACCGGAGCTCTAGAGTCT 102  
 DB 2174 ACCTTGTGTTATCTGGAAGCGGAGAACCAAGAGACCGGAGCTCTAGAGTCT 2233  
 QY 1028 TCGAGGAGGCTATGAGTACTTCTGCGCTCTGCGGAGCCCGCCCAACCGAGATAG 1087  
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 QY 1088 ATTCTGAGCTGTGATGATCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 114  
 DB 2294 ATTCTGAGCTGTGATGATCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 1148 AAGGCTGTGATGATCTGCTGCT 120  
 DB 2344 AAGGCTGTGATGATCTGCTGCT 1273  
 QY 1214 GCTGCTGATCTCTGACATGAGAGCGAGCGCGCTTGTATACCCCATCGCTGGCGAGAAA 1273





1694	TTATCGATTCCCGAGACTCGGAGTCGGTGTATGCGAGAGATGGCCCTCTATGATGTGG	1769
1548	TTTCTCATTCTCTCTGAGCGCGTATGAGGCTCTCTATAGGATTCCTCATACTCTCTTAAGC	607
1754	TCTACCCCTCTCTGAGTGTCTGATGCTGATGGAGGCTCTCATAGGATTCCTCATACTCTCTTAAGC	1813
1608	AGCGGCTCGAGTCTCTGTGTGATCTGAGTGGAGCAAGAAGATGCGCTTGTGGGCTCTCTCAT	667
1814	AGGAGTGGAGTCTCTGTGTGATCTGAGATTCAGAAATCAAGAAGAAACCCCATGGCTTTTCAT	1873
1668	ATGACACCGGCTGTTTTCATCTCGAGTCACTCAGATGATGCATCGTGTATGAGGATCAA	727
1874	ATGTCACATCGCTGTCTGATCTGATCGGCTCAGCAGAGAGATTCGTGTGTGAGGATCAA	1933
728	TTTACCAATCTGTGATCTGATCGGCTCAGCAGAGATTCGTGTGTGAGGATCAA	983
1934	TTTACCAATCTGTGATCTGATCGGCTCAGCAGAGATTCGTGTGTGAGGATCAA	1993
788	GGCTCTGATGAGTGGGCTCTCTATATCTATCTCAAGGAGATTCGTGTGTGAGGATCAA	847
1994	GGCTCTGATGAGTGGGCTCTCTATATCTATCTCAAGGAGATTCGTGTGTGAGGATCAA	2053
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2414	CAGGTAGGACGATCTCAAGTCAACTCTGCTGGTAGGCAACATCATGATATGGCGCCACTT	2473
1268	TGTGGGCAAGATATGATATGATGATCTACTCTCTCTCATCTCTCTTACGCCAAGAGAAC	1327
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1328	TGTGAAGAACCTGGATGTGTAGATCTAGATCTAGCGGGCTGTATCTATCCATGACCACTTAAC	1387
2534	TGTGAAGAACCTGGATGTGTAGATCTAGATCTAGCGGGCTGTATCTATCCATGACCACTTAAC	1447
1388	TACTCTGAGATCATGAAGCATCTCATGCTGATATGAGGATTTTCTACTCATGATATGATGCTC	1447
2594	TACTCTGAGATCATGAAGCATCTCATGCTGATATGAGGATTTTCTACTCATGATATGATGCTC	2653
1448	CAGGTAGATCATGAGGTGGCTTCTTGCTCTGAGAGTCTGGGTACCATCCCTCTGGAG	1507
2654	CAGGTAGATCATGAGGTGGCTTCTTGCTCTGAGAGTCTGGGTACCATCCCTCTGGAG	2713
1508	TGTGGAGATCATGGGCGAGATGTTGCGGCTGCTAGTCTCTCCGAGGAGGAGGCGCG	1567
2714	TGTGGAGATCATGGGCGAGATGTTGCGGCTGCTAGTCTCTCCGAGGAGGAGGCGCG	2773
1568	CCATTGTGGGAAGTACTCTCTCACTGGGAGTAGGACCAAGCTTAAACTACTACTCA	1627

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1688 1688 AGATATATACAGCGCTGCTGCTGCGCCGACCCGCTGGTCTATGTGTGCTTACTCTTAC 1747
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1748 1748 AACTATATACAGCGCTGCTGCTGCGCCGACCCGCTGGTCTATGTGTGCTTACTCTTAC 1793
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```



APPLICANT: FIVE, Inc  
 APPLICANT: MORT, CHALCO  
 APPLICANT: TAKAMIZANA, Akahisa  
 APPLICANT: YOSHIDA, Iwao  
 TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
 SEQUENCE: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Armstrong, Westerman, Hattori, Mclelland &

ADDRESSEE: Naughton

ATTORNEY: 7100 N. 8th St. N. Suite 1000

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0

SOFTWARE: ASCII

CHARACTER SET: ASCII

APPLICATION NUMBER: US/09/315,850

FILING DATE: 09/09/94

PRIOR APPLICATION DATA:

US/08/904,466

FILING DATE: 01-AUG-1991

APPLICATION NUMBER: US 08/324,977

FILING DATE: 18-OCT-1994

PRIOR APPLICATION DATA:

JP 2-167466

FILING DATE: 25-JUN-1990

APPLICATION NUMBER: JP 2-230921

FILING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

JP 3-105605

FILING DATE: 09-NOV-1990

PRIOR APPLICATION DATA:

US 08/099,706

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/769,996

FILING DATE: 28-DEC-1990

PRIOR APPLICATION DATA:

US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

PRIOR APPLICATION DATA:

US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

PRIOR APPLICATION DATA:

US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

PRIOR APPLICATION DATA:

US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

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US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

PRIOR APPLICATION DATA:

US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

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US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

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US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

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US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

FILING DATE: 28-DEC-1990

PRIOR APPLICATION DATA:

US 07/615,451

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/615,451

8 GATGTCATCTCTATCATGACGAGCGCCCTGATCAACGCTGGCTCGCGAGAA 67  
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 1874 ATGACACCGCTCTGTTGACCAAGCTGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAG 1933  
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 1934 TTTACCAATCTGTTGACCAAGCTGCTGAGAGAGCTGAGAGAGCTGAGAGAGCTGAGAG 1993  
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RESULT 9
US-08-904-686A-35
Sequence 35, Application US/08/904686A
Patent No. 5998130
GENERAL INFORMATION:
  INVENTOR: KIMURA, Hiroo
  APPLICANT: FUJIE, Isao
  APPLICANT: MORI, Chisato
  APPLICANT: TAKAMIZAWA, Akahisa
  APPLICANT: ASHIDA, Naoko
  APPLICANT: KAWABATA, Naoko
  TITLE OF INVENTION: NON-B HEPATITIS VIRUS GENOMIC
  TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
  NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
  ADDRESSEE: AMGEN CO.,
  ADDRESS: 1600 AMGEN DRIVE,
  CITY: Thousand Oaks,
  STATE: California,
  COUNTRY: U.S.A.
  STREET: 1725 K St. N.W. Suite 1000
  CITY: Washington
  STATE: D.C.
  COUNTRY: U.S.A.
  ZIP: 20006
COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 3.5 in. 1.44MB
  COMPUTER: IBM PC compatible
  SOFTWARE: FC-500/MS-DOS, Version 5.0
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/904,686A
  FILING DATE: 01-AUG-1997
  PRIORITY DATE: 25-JUN-1996
  APPLICATION NUMBER: US 08/324,977
  FILING DATE: 18-OCT-1994
  PRIORITY DATE: 18-OCT-1994
  APPLICATION NUMBER: JP 2-167466
  FILING DATE: 01-AUG-1997
  PRIORITY DATE: 25-JUN-1996
  APPLICATION NUMBER: JP 2-230921
  FILING DATE: 31-AUG-1990
  PRIORITY DATE: 09-NOV-1990
  APPLICATION NUMBER: US 07/769,996
  FILING DATE: 02-OCT-1991
  PRIORITY DATE: 02-OCT-1991
  APPLICATION NUMBER: US 07/635,451
  FILING DATE: 28-DEC-1990
  PRIORITY DATE: 28-DEC-1990
  ATTORNEY/AGENT INFORMATION:
  NAME: McLeod, Le-Nhung
  ADDRESS: 10000 McLeod Drive, Suite 3141
  CITY: San Diego, CA 92121
  TELEPHONE: (619) 594-1541
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 887-0357
  FAX: (202) 887-0357
  INFO:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 7863 base pairs
  TYPE: nucleic acid
  STRANDNESS: single
  ORIENTATION: 5' to 3'
  MOLECULE TYPE: cDNA from genomic RNA
FEATURES:
  NAME/KEY: CDS
  LOCATION: 1..7863
  FEATURE: misc feature
  NAME/KEY: 1..7863
  LOCATION: 1..7863
  OTHER INFORMATION: /note= "sequence = 1500 - 9162 of

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i. OTHER INFORMATION: SEQ ID NO: 1\*

US-08-904-686A-35

Query Match 88.4%; Score 1593; DB 2; Length 7863;

Best Local Similarity 93.5%; Pred. No. 0;

Matches 1662; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Db 6086 GCGTCCTCATCTCATACATGCACAGCGCGCTTGCATGCCCATGGCTCGCGAGGAGAA 6145

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Db 6146 GCAGCTGCCCATCAACGCGCTGACAGCATCTCTGTCGTCGTCACATCAACCTCGGTCTATT 1205

Qy 128 GCATCATCTCGCGACAGAGCTGCGCGAGAGAGAGTGTACCTTTTCACAGACTGCGCAAG 187

Db 6206 CACAGACTCTCGCGACAGAGCTGCGCGAGAGAGAGTGTACCTTTTCACAGACTGCGCAAG 6265

Qy 188 TCTGAGAGCATCATACCGGACATCTCTGATGGAGATGAGAGAGAGTGTACAGTGTGA 247

Db 6266 TCTGAGAGCATCATACCGGACATCTCTGATGGAGATGAGAGAGAGTGTACAGTGTGA 6325

Qy 248 AGGCTAAATCTGCTATCTGTATGAGAGAGCATCAAGACTGAGGCTCCGCTATCTGGCCAAAT 307

Db 6326 AGGCTAAATCTGCTATCTGTATGAGAGAGCATCAAGACTGAGGCTCCGCTATCTGGCCAAAT 6385

Qy 308 CCAATTTGCTATGTGGGCAAGAGCTTCGAGGCTATACGAGAGGCGGCTTAAACAACA 367

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Qy 368 TCGCTCGTGTGGAAGGACTTCTCTGGAGAGCATGACACCAATTGACACACATCA 427

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Qy 608 AGCGGTGAGTCTCTGATGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667

Db 6688 AGCGGTGAGTCTCTGATGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6745

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Db 7586 TCTGGAGACATCTGGGCGGAGAGTCTCGCGCTAGTCTCTCCGAGGGGGAGGGCGG 1645
Qy 1568 CAAATTTGGCGAGTACTCTTCACTAGCGGAGTAGGACACAGGCTTAACTCTCTCTCA 1627
Db 7646 CAAATTTGGCGAGTACTCTTCACTAGCGGAGTAGGACACAGGCTTAACTCTCTCTCA 1705
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## RESULT 10

US-09-315-850-35

; Sequence 35, Application US/09115850

; Patent No. 6217872

; GENERAL INFORMATION:

; APPLICANT: FUJIE, Isao

; APPLICANT: FUJIE, Isao

; APPLICANT: MORI, Chisato

; APPLICANT: TAKAMIZAMA, Akahisa

; APPLICANT: TORISHITA, Taro

; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDES

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESS: Nuremberg, Westerman, Hattori, McLealand &amp;

; STREET: 1725 K St. N.W. Suite 1000

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMMERCIAL AVAILABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 in., 1.44Mb

; OPERATING SYSTEM: IBM PC compatible

; COMPUTER: PC-DOS/MS-DOS, Version 5.0

; SOFTWARE: ASCII

; CIPHER ALGORITHM DATA:

; APPLICATION NUMBER: US/09/315,850

; FILING DATE: 09/09/1994

; PRIORITY NUMBER: JP 2-167466

; FILING DATE: 20 JUN 1998

; PRIORITY NUMBER: JP 2-230921

; FILING DATE: 31-AUG-1990

; PRIORITY NUMBER: JP 2-305605

; FILING DATE: 09-NOV-1990

; PRIORITY NUMBER: US 08/099,706

; APPLICATION NUMBER: US 07/659,996

; FILING DATE: 02-OCT-1991

; PRIORITY NUMBER: US 07/635,451

; FILING DATE: 28-DEC-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: McLealand, Le-Nhung

; REGISTRATION NUMBER: 31,541

; PRIORITY NUMBER: 07/07030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 659-2930

; TELEFAX: (202) 887-0357

; INFO: US PATENT OFFICE FILE NO. 35;

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7863 base pairs

; TYPE: nucleic acid

; STANDARDS: single

; STANDARDS: single

; MOLECULE TYPE: CDNA from genomic DNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..7863

; NAME/KEY: misc feature

; LOCATION: 1..7863

; OTHER INFORMATION: /note= "sequence = 1500 - 9362 of

; OTHER INFORMATION: SEQ ID NO: 1"

US-09-315-850-35

Query Match 88.4%; Score 1593; DB 3; Length 7863;

Best Local Similarity 93.5%; Pred. No. 0;

Matches 1662; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 8 CAAATTTGGCGAGTACTCTTCACTAGCGGAGTAGGACACAGGCTTAACTCTCTCTCA 67

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Qy 128 CCAAGCTGCCCATCAAGCGGCTGAGCAACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187

Db 6206 CCAACATCTTCCAGAGGAGGCTCTCCGAGAGAGGCTCTCTCTTACAGACTCAG 6265

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Qy 248 AGCGATAGGCTGCTATGAGAGGCTGCTGAGGAGATGAGAGCGAGGCGTCCAGACGCA 307  
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Db 7046 AGCTGCTGATATGAG 7105  
Qy 1028 TCAAGAGAGCTATGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1087  
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Qy 1208 CAGCTAGGAGCACTCAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1267  
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Qy 1508 TCTGGAGAGCTCGGCGAGAGGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1567  
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Qy 1628 TTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1687  
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Qy 1688 AATATATCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1747  
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Db 7826 TCTCGTAGGAGTAAAGGCTCATCTACTCTCCCAACCG 7862

RESULT 11  
US-08-324-997-31 Application US/08324977  
Patent No. 5747339  
GENERAL INFORMATION:  
APPLICANT: OKAYAMA, Hiroko  
INVENTOR: KANE, Hiroko  
APPLICANT: KANE, Hiroko  
APPLICANT: TAKAMIZAWA, Akahisa  
APPLICANT: YOSHIDA, Iwao  
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Naughton  
ADDRESS: 72100 St. N.W. Suite 1000  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB  
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/324,977  
FILING DATE: 18-OCT-1994  
PRIORITY DATE: JP 2-167466  
FILING DATE: 25-JUN-1990  
PRIORITY DATE: JP 2-230921  
FILING DATE: 31-AUG-1990  
PRIORITY DATE: 31-AUG-1990



Db 7646 CCACTGTGGCAATPACTCTTCACTGGGCGTAAACCAACAACTTAACTCACTCCAA 7705  
 Qy 1628 TTCCGCGTGGTCCCGCGTGGCTGGATGTCTGGCGCTGTGTCTGTGGCTAGCGGGGAG 1687  
 Db 7706 TTCCGCGTGGTCCCGCGTGGCTGGATGTCTGGCGCTGTGTCTGTGGCTAGCGGGGAG 7765  
 Qy 1688 ACAATATGACAGCTGTCTGTGGCGGACCCCGCGTGTCTGTGGCTAGCTGTGGCTAG 1747  
 Db 7766 ACAATATGACAGCTGTCTGTGGCGGACCCCGCGTGTCTGTGGCTAGCTGTGGCTAG 7825  
 Qy 1748 TTCTCGTAGGGGTAGGCTGTACTGTACTGTCCCGAAGG 1784  
 Db 7826 TTCTCGTAGGGGTAGGCTGTACTGTACTGTCCCGAAGG 7862

## RESULT 12

US-08-384-616-31

Sequence 31, Application US/08384616

Patent No. 5847101

GENERAL INFORMATION:

APPLICANT: NIMA, Hiroo

APPLICANT: FINE, Isao

APPLICANT: MORI, Chizato

APPLICANT: TAKAMIZAWA, Akahisa

INVENTOR: NIMA, Hiroo

TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESS: Naughton

STREET: 1725 K St. N.W. Suite 1000

CITY: Washington

STATE: D.C.

ZIP: 20005 S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in. 1.44Mb

OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,616

CLASSIFICATION: 424

PRIORITY INFORMATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/769,996

FILING DATE: 02-OCT-1991

PUBLICATION NUMBER: 5,242,467

PILING DATE: 25-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-230921

FILING DATE: 31-AUG-1990

PUBLICATION NUMBER: 5,242,467

PILING DATE: 25-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-305605

FILING DATE: 09-NOV-1990

PUBLICATION NUMBER: 5,242,467

PILING DATE: 25-JUN-1990

ATTORNEY/AGENT INFORMATION:

NAME: Stevens-Smith, Theresa M.

REGISTRATION NUMBER: 36,281

TELEPHONE: (202) 659-2930

TELEFAX: (202) 887-0357

FLEX: 440442

INFORMATION ID. NO. 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 7917 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPLOGY: linear

; MOLECULE TYPE: cDNA from genomic RNA  
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 US-08-384-616-31

Query Match 88.4%; Score 1593; DB 2; Length 7917;  
 Best Local Similarity 91.5%; Pred. No. 0;  
 Matches 1662; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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QY 908 CGCGGCGAGCGGGCTGTCAGAGCTAGTGGGATATACCTCAGATCTACTTGAAG 967
DB 6986 CCGCTGCTAGCTGTCAGAGCTCTGAGAGCTGAGAGCTGAGAGCTGAGAGAG 7045
QY 968 ACTCTGCTGATCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
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DB 7236 AAGGGTGTAATCTACTCTACCGCTGATCCACACACCCCTAGCACGGCTGCTGGAGAGA 7295
QY 1208 CAGTGAGCAGCATCATGATCATCTGAGCTGAGCAGATCATCATCATCATCATCATCAT 1267
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QY 1448 CAGTGAGATCATTAAGGCTCTCATGCTCTCAGAGAGCTTGGGGTGCACCCCTTCGGAG 1507
DB 7526 CAGTGAGATCATTAAGGCTCTCATGCTCTCAGAGAGCTTGGGGTGCACCCCTTCGGAG 7585
QY 1508 TCTGGAGACATCGGCGCAGAGAGCTGCTGCGCTTAAGTACTCTCCAGCGGGGAGAGGCG 1567
DB 7586 TCTGGAGACATCGGCGCAGAGAGCTGCTGCGCTTAAGTACTCTCCAGCGGGGAGAGGCG 7645
QY 1568 CAGTTGTGGCAGTACTCTCTCAACTGGCAGTAGAGCAACAGCTTAACTCACTCCAA 1627
DB 1626 CAGTTGTGGCAGTACTCTCTCAACTGGCAGTAGAGCAACAGCTTAACTCACTCCAA 7705
QY 1628 TCTCGAGCTGGGCTGCGGCTGCACTGCTGCGCTGGTCTGGTCTGCTGCTGCTGCTGCTG 1687
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RESULT 14
US-10-712-479-31
Sequence 31
Application US/09315850
Patent No. 6217872
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
INVENTOR: OKAYAMA, Hiroto
APPLICANT: OKI, Chisato
APPLICANT: TAKEMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSES: Armstrong, Westerman, Hattori, McEland &
1725 K Street, N.W. Suite 1000
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09315,850

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APPLICATION NUMBER: US 08/904,686  
 FILING DATE: 31-AUG-1997  
 PRIOR APPLICATION NUMBER: 08/7324,977  
 FILING DATE: 18-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-167466  
 FILING DATE: 29-AUG-1990  
 PRIOR APPLICATION NUMBER: JP 2-210321  
 FILING DATE: 31-AUG-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 2-305005  
 FILING DATE: 09-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/099,706  
 FILING DATE: 10-JUL-1993  
 PRIOR APPLICATION NUMBER: US 07/769,996  
 FILING DATE: 02-OCT-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/635,451  
 FILING DATE: 29-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McLeiland, Le-Nhung  
 REGISTRATION NUMBER: 31,541  
 REFERENCE NUMBER: 900703G  
 TELEPHONE: (202) 659-2930  
 TELEFAX: (202) 887-0357  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7917 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE: CDS  
 FEATURE TYPE: CDS from genomic RNA  
 NAME/KEY: CDS  
 LOCATION: 1..7862  
 FEATURE:  
 NAME/KEY: nice feature  
 LOCATION: 1..7916  
 OTHER INFORMATION: /notes="sequence = 1500 - 9416 of  
 OTHER INFORMATION: SEQ ID NO: 1"  
 US-09-315-850-31

Query Match 88.4%; Score 1593; DB 3; Length 7917;  
 Best Local Similarity 93.5%; Pred. Loc. 0;  
 Matches 1662; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 8 GCGATGATGATCTTATACATGACGAGCGCCCTGATCAACCGTGGCGTGGCGGAAH 67  
 DB 6086 GTCTCTCATGTTCTTACATACATGACGAGCGCCTGATCAAGCCATGCGCTCGAGGAAH 6145  
 QY 68 GCGATGATGATCTTATACATGACGAGCGCCCTGATCAACCGTGGCGTGGCGGAAH 127  
 DB 6146 GCGATGATGATCTTATACATGACGAGCGCCTGATCAAGCCATGCGCTCGAGGAAH 6205  
 QY 128 CCAACATCTCCGAGCGCGCCCTGCGGAGAGAGAGTGCATCTTTACACAGATCGAAG 187  
 DB 6206 CCGAATCTCCGAGCGCGCCCTGCGGAGAGAGAGTGCATCTTTACACAGATCGAAG 6265  
 QY 188 TCTCTGACATGATTAACCGGAGCGCGCTGATCAAGCGATGAGGAGCGGCTCCACAGTA 247  
 DB 6266 TCTGAGAGAGCTACCGGAGCGCGCTGATCAAGCGATGAGGAGCGGCTCCACAGTA 6325  
 QY 248 AGGCTAAAGTCTATCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307  
 DB 6326 AGGCTAAAGTCTATCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6385  
 QY 308 CCAATTTGGGCTATGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367  
 DB 6386 CCAATTTGGGCTATGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6445

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 DB 6446 TCCCTCTCCCTGTGGAGAGACTTCTGTGGAGAGACTTCAACACCAATTCAGACCAACATCA 4505  
 QY 428 TGGCAAAAATGAGGTTTCTGTCTCAACAGAGAAAGAGAGCGGCGGAAACCAAGCTGCC 487  
 DB 6506 TGGCAAAAATGAGGTTTCTGTCTCAACAGAGAAAGAGAGCGGCGGAAACCAAGCTGCC 4855  
 QY 488 TCAATGATTTCCAGACACTCGGAGTCTGTATTCGAGAGAGAGAGCGGCTTACAGCTGG 544  
 DB 6566 TCAATGATTTCCAGACACTCGGAGTCTGTATTCGAGAGAGAGAGCGGCTTACAGCTGG 6625  
 QY 548 TTTCCATCTCTCTCAGCGCTGATGGGCTCTCTATACGAGTTCCGATCTCTCTTAAGC 607  
 DB 6626 TTTCCATCTCTCTCAGCGCTGATGGGCTCTCTATACGAGTTCCGATCTCTCTTAAGC 6685  
 QY 608 AGCGAGTCTGCTGCTGATCTGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667  
 DB 6686 AGCGAGTCTGCTGCTGATCTGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6745  
 QY 668 ATGACGCTGCTGCTGATCTGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727  
 DB 6746 ATGACGCTGCTGCTGATCTGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6805  
 QY 728 TTTACCAATGTTTGAATCTTGGGCTCTGAGCTACAGAGGCGATTAAGCTCTCTCAGAGC 787  
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 QY 908 CCGCTGCGAGCCTCTGAGCTCGAGACTCCAGAGCTCCAGATGCTGAATGAGAGC 967  
 DB 6986 CCGCTGCGAGCCTCTGAGCTCGAGACTCCAGAGCTCCAGATGCTGAATGAGAGC 7045  
 QY 968 AGCTGCTGCTTATCTGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027  
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 QY 1028 TACAGAGGCTATGATCTAGTACTCTGCGCTCTGCGGAGAGAGAGAGAGAGAGAGAG 1087  
 DB 7106 TACAGAGGCTATGATCTAGTACTCTGCGCTCTGCGGAGAGAGAGAGAGAGAGAGAG 7165  
 QY 1088 ACTTGGAGCTTAACATGCTGCTTCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1147  
 DB 7166 ACTTGGAGCTTAACATGCTGCTTCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7225  
 QY 1148 AAGAGGCTGATCACTCAAGCGCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1207  
 DB 7226 AAGAGGCTGATCACTCAAGCGCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7285  
 QY 1208 CAGCTAGGAGCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267  
 DB 7286 CAGCTAGGAGCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7345  
 QY 1268 TGTGGGAGAGATGATTTGATGATCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1327  
 DB 7346 TGTGGGAGAGATGATTTGATGATCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7405  
 QY 1328 TGTGAGAGCTGATTTGATGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1387  
 DB 7406 TGTGAGAGCTGATTTGATGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7465  
 QY 1388 TCTGAGAGCTGATTTGATGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447  
 DB 7466 TCTGAGAGCTGATTTGATGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7525

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Oy 1448 CAGGTGAGTCAATAGGCTGGCTTCACTGCTCAGGAGCTTGGGTACACCTCTGGAG 1507
Db 7526 CAGGTGAGTCAATAGGCTGGCTTCACTGCTCAGGAGCTTGGGTACACCTCTGGAG 1585
Oy 1508 TCTGGAGACATGGGCGAGAGGTGCTCGGGCTAAGTCTACTGTCGCCAGGGGGGGGGCG 1567
Db 7586 TCTGGAGACATGGGCGAGAGGTGCTCGGGCTAAGTCTACTGTCGCCAGGGGGGGGGCG 1645
Oy 1568 TCTGGAGACATGGGCGAGAGGTGCTCGGGCTAAGTCTACTGTCGCCAGGGGGGGGGCG 1627
Db 7646 CCACTCTGGGCAATTAACCTTCTTCACTGCGGACGTAAAGCTTAACCTCACTCAA 1705
Oy 1628 TCTGGAGACATGGGCGAGAGGTGCTCGGGCTAAGTCTACTGTCGCCAGGGGGGGGGCG 1687
Db 7706 TCCGGCTGGCTCGGGCTAAGTCTACTGTCGCCAGGGGGGGGGGGGGGGGGGGGG 1765
Oy 1688 ACAATTAACAGAGCTGCTCTGTCGGCGACCGGGCGGTGCTAAGTGTGGCTACTCTAC 1747
Db 7766 ACAATTAACAGAGCTGCTCTGTCGGCGACCGGGCGGTGCTAAGTGTGGCTACTCTAC 1825
Oy 1748 TCTCGGTAGGCTAGGCTACTTACTCTCCCAACCG 1784
Db 7826 TTTCTGAGGGGTAGGCTACTTACTCTCCCAACCG 7862

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## RESULT 15

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US-08-324-977-13
Sequence 13
GENERAL INFORMATION US/08324977
GENERAL INFORMATION:
APPLICANT: OXAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: KAWABATA, Shiro
APPLICANT: TAKAMIZAWA, Akihisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CNA AND ANTIGEN POLYPEPTIDE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amstrong, Westernman, Hattori, Mclelland &
ADDRESSES: Naughton
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER: IBM PC compatible
MEDIUM TYPE: Diskette, 3.5 in., 1.44MB
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
COMPUTER DATA:
APPLICATION NUMBER US/08/324,977
FILING DATE: 18-OCT-1994
PRIORITY DATE:
APPLICATION NUMBER: JP 2-167466
PRIORITY DATE: 09-NOV-1990
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIORITY DATE:
APPLICATION NUMBER: US 07/659,996
FILING DATE: 02-OCT-1991
PRIORITY DATE:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 25-SEP-1990

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: NAME: Stevens-Smith, Theresa M.
: REGISTRATION NUMBER: 36,281
: REFERENCE/DOCKET NUMBER: 900703D
: TELEPHONE: (202) 659-2930
: TELEFAX: (202) 887-0357
: TELEX: 440142
: INFORMATION FOR SEQ. ID NO. 13:
: SEQUENCE LENGTH: 9030 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: MOLECULE TYPE: linear
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 1..9030
: OTHER INFORMATION: SEQ ID NO. 1"
: NAME/KEY: CDS
: LOCATION: 1..9030
: US-08-324-977-13

Query Match
Best Local Similarity 88.4%; Score 1593; DB 1; Length 9030;
Matches 1662; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

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Oy 608 AGCGGTGGGTCTCTCTGATTAACCTGGAAGAGAGAAATGCTATGAGGCTTCTCAT 667
Db 7853 AGCGGTGGGTCTCTCTGATTAACCTGGAAGAGAGAAATGCTATGAGGCTTCTCAT 7912

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Db	7913	ATGACATCCGCTGTTTGCACTCCAGAGGTCACGACGACATCCGTTGTAGAGATCAA	7972	TTTCTGTAGGGGTAGGCACTTACCTGCTCCCAACG	8993	TTTCTGTAGGGGTAGGCACTTACCTGCTCCCAACG
Qy	7928	TTATCAATGTTGTGATCTGGCCCGGAGCTAGAGAGGCCATAGTGTCTCCAGAGAC	7987	TTATCAATGTTGTGATCTGGCCCGGAGCTAGAGAGGCCATAGTGTCTCCAGAGAC		
Db	7973	TTATCAATGTTGTGATCTGGCCCGGAGCTAGAGAGGCCATAGTGTCTCCAGAGAC	8032	TTATCAATGTTGTGATCTGGCCCGGAGCTAGAGAGGCCATAGTGTCTCCAGAGAC		
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Qy	908	CGGCTGCGAGCTGT	967	CGGCTGCGAGCTGT		
Db	8153	CGGCTGCGAGCTGT	8212	CGGCTGCGAGCTGT		
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Qy	1028	TGACGGAGGCTATGCTGT	1087	TGACGGAGGCTATGCTGT		
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Db	8333	ACTTGTGAGCTGT	8392	ACTTGTGAGCTGT		
Qy	1148	TAAGGGGT	1207	TAAGGGGT		
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Db	8813	CAATTTGT	8872	CAATTTGT		
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7-5-2012